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(54) FURTHER NOVEL FORMS OF INTERFERING RNA MOLECULES

WEITERE NEUE FORMEN VON INTERFERIERENDE RNS MOLEKÜLE

NOUVELLES FORMES DE MOLECULES D'ARN INTERFERANT

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Description

[0001] The present invention is related to a ribonucleic acid comprising a double-stranded structure whereby the double-stranded structure comprises a first strand and a second strand, whereby the first strand comprises a first stretch 5 of contiguous nucleotides and whereby said first stretch is at least partially complementary to the target nucleic acid, and the second strand comprises a second stretch of contiguous nucleotides whereby said second stretch is at least partially identical to a target nucleic acid, the use of such ribonucleic acid, a cell and an organism, respectively, comprising such ribonucleic acid, a composition containing such ribonucleic acid, a pharmaceutical composition containing such ribonucleic acid and a method for inhibiting expression of a targeted gene.

[0002] RNA-mediated interference (RNAi) is a post-transcriptional gene silencing mechanism initiated by double stranded RNA (dsRNA) homologous in sequence to the silenced gene (Fire (1999), Trends Genet 15, 358-63, *Tuschl*, *et al.* (1999), Genes Dev 13, 3191-7, , Waterhouse, *et al.* (2001), Nature 411, 834-42, Elbashir, *et al.* (2001), Nature 411, 494-8, for review see Sharp (2001), Genes Dev 15, 485-90, Barstead (2001), Curr Opin Chem Biol 5, 63-6). RNAi has been used extensively to determine gene function in a number of organisms, including plants (Baulcombe (1999), 10 Curr Opin Plant Biol 2, 109-13), nematodes (Montgomery, *et al.* (1998), Proc Natl Acad Sci U S A 95, 15502-7), *Drosophila* (Kennerdell, *et al.* (1998), Cell 95, 1017-26, Kennerdell, *et al.* (2000), Nat Biotechnol 18, 896-8). In the nematode *C. elegans* about one third of the genome has already been subjected to functional analysis by RNAi (Kim (2001), Curr Biol 11, R85-7, Maeda, *et al.* (2001), Curr Biol 11, 171-6).

[0003] Until recently RNAi in mammalian cells was not generally applicable, with the exception of early mouse development (Wianny, *et al.* (2000), Nat Cell Biol 2, 70-5). The discovery that transfection of duplexes of 21-nt into mammalian cells interfered with gene expression and did not induce a sequence independent interferon-driven anti-viral response usually obtained with long dsRNA led to new potential application in differentiated mammalian cells (Elbashir *et al.* (2001), Nature 411, 494-8). Interestingly these small interfering RNAs (siRNAs) resemble the processing products from long dsRNAs suggesting a potential bypassing mechanism in differentiated mammalian cells. The Dicer complex, a 20 member of the RNase III family, necessary for the initial dsRNA processing has been identified (Bernstein, *et al.* (2001), Nature 409, 363-6, Billy, *et al.* (2001), Proc Natl Acad Sci U S A 98, 14428-33). One of the problems previously encountered when using unmodified ribooligonucleotides was the rapid degradation in cells or even in the serum-containing medium (Wickstrom (1986), J Biochem Biophys Methods 13, 97-102, Cazenave, *et al.* (1987), Nucleic Acids Res 15, 10507-21). It will depend on the particular gene function and assay systems used whether the respective knock down induced by 25 transacted siRNA will be maintained long enough to achieve a phenotypic change.

[0004] Parrish S. *et al.* (Molecular Cell, vol. 6, 1077-1087, November, 2005) describe the requirements of dsRNAs targeting the *C. elegans* unc 22 gene. More specifically, the impact of chemical modification of distinct nucleotides is investigated, whereby whether a nucleotide is modified depends on the chemical nature of the nucleotide.

[0005] Published international patent application WO 02/055693 discloses the use of RNAi molecules having a double-stranded structure, whereby such RNAi molecules have an overhang on one end formed by 1-4 nucleotides.

[0006] Published international patent application WO 02/044321 discloses the use of RNAi molecules having a double-stranded structure, whereby such RNAi molecules have a length of 19-23 nucleotide pairs.

[0007] Published international patent application WO 95/13834 discloses chimeric oligonucleoside compounds which are useful in activating RNAase H-mediated cleavage of target nucleic acid sequences. More specifically, such chimeric oligonucleoside compounds are single-stranded oligonucleotides which are complementary to a target nucleic acid.

[0008] The problem underlying the present invention was to provide synthetic interfering RNA molecules which are both stable and active in a biochemical environment such as a living cell.

[0009] The problem underlying the present invention is solved by the subject matter of the attached independent claims. Preferred embodiments may be taken from the attached dependent claims.

[0010] The present invention is based on the surprising finding that small interfering RNAs can be designed such as to be both highly specific and active as well as stable under the reaction conditions typically encountered in biological systems such as biochemical assays or cellular environments. The various interfering RNAs described in the prior art such as by Tuschl *et al.* (international patent application WO 01/75164) provide for a length of 21 to 23 nucleotides and a modification at the 3' end of the double-stranded RNA. It has been surprisingly found by the present inventors that the problem of stability of interfering RNA, including small interfering RNA (siRNA) which is generally referred to herein in the following as RNAi, actually resides in the attack of endonucleases rather than exonucleases as thought earlier. Based on this finding several strategies have been perceived by the present inventors which are subject to the present application.

[0011] The present invention is thus related to new forms of interfering RNA as defined in claim 1. RNAi consists of a ribonucleic acid comprising a double-stranded structure. Said double-stranded structure is formed by a first strand and a second strand. Said first strand comprises a stretch of contiguous nucleotides, also referred to as first stretch of contiguous nucleotides herein, and this first stretch is at least partially complementary to a target nucleic acid. Said second strand comprises also a stretch of contiguous nucleotides whereby said second stretch is at least partially

identical to a target nucleic acid. The very basic structure of this ribonucleic acid is schematically shown in Fig. 1. Said first strand and said second strand are preferably hybridised to each other and form the double-stranded structure. The hybridisation typically occurs by Watson Crick base pairing. The inventive ribonucleic acid, however, is not necessarily limited in its length to said double-stranded structure. There might be further nucleotides added to each strand and/or to each end of any of the strands forming the RNAi. Depending on the particular sequence of the first stretch and the second stretch, the hybridisation or base pairing is not necessarily complete or perfect, which means that the first and the second stretch are not 100 % base paired due to mismatches. There might also be one or more mismatches within the duplex. Said mismatches have no effect on the RNAi activity if placed outside a stretch of preferably 15, 16 or 17 matching nucleotides. If mismatches are placed to yield only 15 or less contiguous matching nucleotides, the RNAi molecule typically shows a reduced activity in down regulating mRNA for a given target compared to a 17 matching nucleotide duplex.

[0012] The first stretch of contiguous nucleotides of the first strand is essentially complementary to a target nucleic acid, more preferably to a part of the target nucleic acid. Complementary as used herein preferably means that the nucleotide sequence of the first strand is hybridising to a nucleic acid sequence of a target nucleic acid sequence or a part thereof. Typically, the target nucleic acid sequence or target nucleic acid is, in accordance with the mode of action of interfering ribonucleic acids, a single stranded RNA, more preferably an mRNA. Such hybridisation occurs most likely through Watson Crick base pairing, however, is not necessarily limited thereto. The extent to which said first strand and more particularly the first stretch of contiguous nucleotides of said first strand is complementary to a target nucleic acid sequence can be as high as 100% and be as little as 80%, preferably 80-100%, more preferably 85-100%, most preferably 90-100%. Optimum complementarity seems to be 95-100%. Complementarity in this sense means that the aforementioned range of nucleotides, such as, e. g., 80%-100%, depending on the particular range, of the nucleotides are perfect by Watson Crick base pairing. It is shown in one aspect of the present invention that the complementarity between said first stretch of nucleotides and the target RNA has to be 18-19 nucleotides, stretches of as little as 17 nucleotides even with two sequence specific overhangs are not functional in mediating RNAi. Accordingly, given a duplex having a length of 19 nucleotides or base pairs a minimum complementarity of 17 nucleotides or nucleotide base pairs would be acceptable allowing for a mismatch of two nucleotides. In case of a duplex consisting of 20 nucleotides or base pairs a complementarity of 17 nucleotides or nucleotide base pairs would be allowable and functionally active. The same applies to a duplex of 21 nucleotides or base pairs with a total of 17 complementary nucleotides or base pairs. Basically, the extent of complementarity required for a length of a duplex, i. e. of a double stranded structure, can also be based on the melting temperature of the complex formed by either the double stranded structure as described herein or by the complex of the first stretch of the first strand and the target nucleic acid.

[0013] It is to be understood that all of the ribonucleic acids of the present invention are suitable to cause or being involved in RNA mediated interference such as, for example, described in international patent applications WO 99/32619, WO 00/44895 and WO 01/75164.

[0014] The first strategy according to which an interfering ribonucleic acid molecule in accordance with claim 1 may be designed according to the present invention is to have an optimum length of 18 or 19 nucleotides of the stretch which is complementary to the target nucleic acid. It is also within the present invention that said optimum length of 18 or 19 nucleotides is the length of the double stranded structure in the RNAi used. This length requirement is clearly different from the technical teaching of the prior art such as, for example, international patent application WO 01/75164. It is within the present invention that any further design, both accenting to the present invention and as described in the prior art, can be realised in connection with an interfering ribonucleic acid having said length characteristics, i.e. a length of 18 or 19 nucleotides.

[0015] The second strategy according to which an interfering ribonucleic acid molecule in accordance with claim 1 may be designed is to have a free 5' hydroxyl group, also referred to herein as free 5' OH-group, at the first strand. A free 5' OH-group means that the most terminal nucleotide forming the first strand is present and is thus not modified, particularly not by an end modification. Typically, the terminal 5'-hydroxy group of the second strand, respectively, is also present in an unmodified manner. In a more preferred embodiment, also the 3'-end of the first strand and first stretch, respectively, is unmodified such as to present a free OH-group which is also referred to herein as free 3'OH-group, whereby the design of the 5' terminal nucleotide is the one of any of the aforementioned embodiments. Preferably such free OH-group is also present at the 3'-end of the second strand and second stretch, respectively. In other embodiments of the ribonucleic acid molecules as described previously according to the present invention the 3'-end of the first strand and first stretch, respectively, and/or the 3'-end of the second strand and second stretch, respectively, may have an end modification at the 3' end.

[0016] As used herein the terms free 5'OH-group and 3'OH-group also indicate that the respective most terminal nucleotide at the 5' end and the 3' end of the polynucleotide, respectively, presents an OH-group. Such OH-group may stem from either the sugar moiety of the nucleotide, more preferably from the 5'position in case of the 5'OH-group and from the 3'position in case of the 3'OH-group, or from a phosphate group attached to the sugar moiety of the respective terminal nucleotide. The phosphate group may in principle be attached to any OH-group of the sugar moiety of the

nucleotide. Preferably, the phosphate group is attached to the 5'OH-group of the sugar moiety in case of the free 5'OH-group and/or to the 3'OH-group of the sugar moiety in case of the free 3'OH-group still providing what is referred to herein as free 5' or 3' OH-group.

[0017] As used herein with any strategy for the design of RNAi or any embodiment of RNAi disclosed herein, the term 5 end modification means a chemical entity added to the most 5' or 3' nucleotide of the first and/or second strand. Examples for such end modifications include, but are not limited to, inverted (deoxy) abasics, amino, fluoro, chloro, bromo, CN, CF, methoxy, imidazole, carboxylate, thioate, C₁ to C₁₀ lower alkyl, substituted lower alkyl, alkaryl or aralkyl, OCF₃, OCN, O-, S-, or N-alkyl; O-, S-, or N-alkenyl; SOCH₃; SO₂CH₃; ONO₂; NO₂, N₃; heterocycloalkyl; heterocycloalkaryl; aminoalkylamino; polyalkylamino or substituted silyl, as, among others, described in European patents EP 0 586 520 B1 or EP 0 618 925 B1.

[0018] As used herein, alkyl or any term comprising "alkyl" means any carbon atom chain comprising 1 to 12, preferably 1 to 6 and more, preferably 1 to 2 C atoms.

[0019] A further end modification is a biotin group. Such biotin group may preferably be attached to either the most 5' or the most 3' nucleotide of the first and/or second strand or to both ends. In a more preferred embodiment the biotin 15 group is coupled to a polypeptide or a protein. It is also within the scope of the present invention that the polypeptide or protein is attached through any of the other aforementioned end modifications. The polypeptide or protein may confer further characteristics to the inventive nucleic acid molecules. Among others the polypeptide or protein may act as a ligand to another molecule. If said other molecule is a receptor the receptor's function and activity may be activated by the binding ligand. The receptor may show an internalization activity which allows an effective transfection of the ligand 20 bound inventive nucleic acid molecules. An example for the ligand to be coupled to the inventive nucleic acid molecule is VEGF and the corresponding receptor is the VEGF receptor.

[0020] Various possible embodiments of the RNAi of the present invention having different kinds of end modification (s) are presented in the following table 1.

25 Table 1: Various embodiments of the interfering ribonucleic acid according to the present **invention**

	1 st strand/1 st stretch	2 nd strand/ 2 nd stretch
1.) 5'-end	free OH	free OH
3'-end	free OH	free OH
2.) 5'-end	free OH	free OH
3'-end	end modification	end modification
3.) 5'-end	free OH	free OH
3'-end	free OH	end modification
4.) 5'-end	free OH	free OH
3'-end	end modification	free OH
5.) 5'-end	free OH	end modification
3'-end	free OH	free OH
6.) 5'-end	free OH	end modification
3'-end	end modification	free OH
7.) 5'-end	free OH	end modification
3'-end	free OH	end modification
8.) 5'-end	free OH	end modification
3'-end	end modification	end modification

[0021] The various end modifications as disclosed herein are preferably located at the ribose moiety of a nucleotide of the ribonucleic acid. More particularly, the end modification may be attached to or replace any of the OH-groups of the ribose moiety, including but not limited to the 2'OH, 3'OH and 5'OH position, provided that the nucleotide thus modified is a terminal nucleotide. Inverted abasics are nucleotides, either desoxyribonucleotides or ribonucleotides which do not have a nucleobase moiety. This kind of compound is, among others, described in Sternberger et al.(2002), Antisense. Nucl. Ac. Drug Dev. in press.

[0022] Any of the aforementioned end modifications may be used in connection with the various embodiments of RNAi 50 depicted in table 1. In connection therewith it is to be noted that any of the RNAi forms or embodiments disclosed herein with the sense strand being inactivated, preferably by having an end modification more preferably at the 5' end, are particularly advantageous. This arises from the inactivation of the sense strand which corresponds to the second strand of the ribonucleic acids described herein, which might otherwise interfere with an unrelated single-stranded RNA in the cell. Thus the expression and more particularly the translation pattern of the transcriptome of a cell is more specifically

influenced. This effect is also referred to as off-target effect. Referring to table 1 those embodiments depicted as embodiments 7 and 8 are particularly advantageous in the above sense as the modification results in an inactivation of the - target unspecific - part of the RNAi (which is the second strand) thus reducing any unspecific interaction of the second strand with single-stranded RNA in a cellular or similar system where the RNAi according to the present invention is going to be used to knock down specific ribonucleic acids and proteins, respectively.

[0023] A third strategy subject to the present invention is to realise a ribonucleic acid in accordance with claim 1 comprising a double-stranded structure whereby the double-stranded structure comprises a first strand and a second strand, whereby the first strand comprises a first stretch of contiguous nucleotides and whereby said first stretch is at least partially to a target nucleic acid, and the second strand comprises a second stretch of contiguous nucleotides whereby said second stretch is at least partially identical to a target nucleic acid whereby the double-stranded structure is blunt-ended. As used in connection with the present description the term double-stranded structure is also referred to as duplex. This design of RNAi is thus clearly different from, e. g., the one of Tuschl et al. as specified in patent application WO 01/75164 which discloses a 3'-overhang. As used herein overhang refers to a double-stranded structure whereby at least one end of one strand is longer than the corresponding end of the other strand forming the double-stranded structure, which is also referred to herein as the counter strand. Preferably, the first stretch is identical to the first strand and the second stretch is identical to the second strand.

[0024] Taken the effectiveness of blunt-ended RNAi and the advantages of an end modification of either the first or the second strand or both, respectively, of the respective ribonucleic acid it is preferred to have a combination of both design principles. In other words, it is within the present invention to have blunt-ended RNAi carrying any end modification scheme as depicted in table 1.

[0025] The fourth strategy subject to the present invention is to have an overhang at the 5'-end of the ribonucleic acid in accordance with claim 1. More particularly, such overhang may in principle be present at either or both the first strand and second strand of the ribonucleic acid according to the present invention. The length of said overhang may be as little as one nucleotide and as long as 2 to 8 nucleotides, preferably 2, 4, 6 or 8 nucleotides. It is within the present invention that the 5' overhang may be located on the first strand and/or the second strand of the ribonucleic acid according to the present application. The nucleotide(s) forming the overhang may be (a) desoxyribonucleotide(s), (a) ribonucleotide(s) or a continuation thereof.

[0026] The overhang preferably comprises at least one desoxyribonucleotide, whereby said one desoxyribonucleotide is preferably the most 5'-terminal one. It is within the present invention that the 3'-end of the respective counter-strand of the inventive ribonucleic acid does not have an overhang, more preferably not a desoxyribonucleotide overhang. Here again, any of the inventive ribonucleic acids may comprise an end modification scheme as outlined in connection with table 1 and/or and end modification as outlined herein.

[0027] The strategy in the design of interfering ribonucleic acids in accordance with claim 1 resides in the formation of a certain pattern of modified nucleotides on both the first and the second and more particularly on both the first and the second stretch of contiguous nucleotides of the ribonucleic acid(s) according to the present invention. The kind of modification of said nucleotides may be the same as discussed in connection with the other strategies for designing interfering RNA as disclosed herein and more particularly the kind of modification described herein for or as an end modification, such as, e.g., inverted abasics, methoxy, or amino and the like at the ribose moiety of at least one nucleotide forming the ribonucleotide acids according to the present application. It is to be noted that the modification of said nucleotides may be any form of modification described herein, more particularly the kind of modification as described herein as end modification with the par that the so-caused end modification is not necessarily located at terminal nucleotides. Rather the modification is occurring at a non-terminal nucleotide. Under such conditions the modification is preferably attached to the ribose moiety of the - to be - modified nucleotide and even more preferably to the 2'-position of the ribose moiety.

[0028] It is also within the present invention that any ribonucleic acid in accordance with claim 1 may also have the features conferred to a ribonucleic acid in accordance with claim 1 by any of the other design strategies disclosed herein. Accordingly, the interfering ribonucleic acid having a pattern of modified nucleotides may have an end modification, an end modification scheme, may be blunt ended or may have a 5' overhang or any combination of two or more of these elements or characteristics.

[0029] Apart from the aforementioned modifications which may be presented either as end modifications or as modification pattern, the ribonucleic acid backbone as such may be further modified by forming different links between the nucleotides. Such different links are, among others, described in European patent EP 0 586 520 B1 and European patent EP 0 618 925 B1. Of particular interest here are internal modification(s) of the ribonucleic acid backbone which have been shown to confer higher nuclease resistance of ribooligonucleotides. In a preferred embodiment the modification of the modified nucleotide is a methylation of the 2'-OH-group of the ribose moiety of the nucleotide.

[0030] In accordance with claim 1 both strands, and more particularly both the first stretch and the second stretch show this kind of modification of the nucleotides forming said strands and stretches, respectively. As used herein, the term group of modified nucleotide or flanking group of nucleotide may comprise or represent as little nucleotides as one

nucleotide, i. e. one or more nucleotides.

[0031] Taken the stretch of contiguous nucleotides a pattern of modification of the nucleotides forming the stretch may be realised such that a single nucleotide or group of nucleotides which are covalently linked to each other via standard phosphorodiester bonds or, at least partially, through phosphorothioate bands, show such kind of modification.

5 In case such nucleotide or group of nucleotides which is also referred to herein as group of modified nucleotides, is not forming the 5'-end or 3'-end of said stretch a nucleotide or group of nucleotides follows on both sides of the nucleotide which does not have the modification of the preceding nucleotide or group of nucleotides. It is to be noted that this kind of nucleotide or group of nucleotides, however, may have a different modification. This kind of nucleotide or group of nucleotides is also referred to herein as the flanking group of nucleotides. This sequence of modified nucleotide and group of modified nucleotides, respectively, and unmodified or differently modified nucleotide or group of unmodified or differently modified nucleotides may be repeated one or several times. Preferably, the sequence is repeated more than one time. For reason of clarity the pattern is discussed in more detail in the following, generally referring to a group of modified nucleotides or a group of unmodified nucleotides whereby each of said group may actually comprise as little as a single nucleotide. Unmodified nucleotide as used herein means either not having any of the afore-mentioned modifications at the nucleotide forming the respective nucleotide or group of nucleotides, or having a modification which is different from the one of the modified nucleotide and group of nucleotides, respectively.

10 **[0032]** It is also within the present invention that the modification of the unmodified nucleotide(s) wherein such unmodified nucleotide(s) is/are actually modified in a way different from the modification of the modified nucleotide(s), can be the same or even different for the various nucleotides forming said unmodified nucleotides or for the various flanking groups of nucleotides.

15 **[0033]** The pattern of modified and unmodified nucleotides may be such that the 5'-terminal nucleotide of the strand or of the stretch starts with a modified group of nucleotides or starts with an unmodified group of nucleotides. However, in an alternative embodiment it is also possible that the 5'-terminal nucleotide is formed by an unmodified group of nucleotides.

20 **[0034]** This kind of pattern may be realised either on the first stretch or the second stretch of the interfering RNA or on both. It has to be noted that a 5' phosphate on the target-complementary strand of the siRNA duplex is required for siRNA function, suggesting that cells check the authenticity of siRNAs through a free 5' OH (which can be phosphorylated) and allow only such bona fide siRNAs to direct target RNA destruction (Nykanen, *et al.* (2001), Cell 107, 309-21).

25 **[0035]** It is within the present invention that both the first stretch and the second stretch have this kind of pattern. Preferably, the pattern of modification and non-modification is the same for both the fast stretch and the second stretch.

30 **[0036]** In a preferred embodiment the group of nucleotides forming the second stretch and corresponding to the modified group of nucleotides of the first stretch are also modified whereas the unmodified group of nucleotides of or forming the second stretch correspond to the unmodified group of nucleotides of or forming the first stretch. This possibility is schematically depicted in Fig. 2A. Another alternative is that there is a phase shift of the pattern of modification of the first stretch and first strand, respectively, relative to the pattern of modification of the second stretch and second strand, respectively. Preferably, the shift is such that the modified group of nucleotides of the first strand corresponds to the unmodified group of nucleotides of the second strand and vice versa. This possibility is shown in Fig. 2B. It is also within the present invention that the phase shift of the pattern of modification is not complete but overlapping as illustrated in Fig. 2C.

35 **[0037]** In a preferred embodiment the second nucleotide at the terminus of the strand and stretch, respectively, is an unmodified nucleotide or the beginning of group of unmodified nucleotides. Preferably, this unmodified nucleotide or unmodified group of nucleotides is located at the 5'-end of the first and second strand, respectively, and even more preferably of the first strand. In a further preferred embodiment the unmodified nucleotide or unmodified group of nucleotide is located at the 5'-end of the first strand and first stretch, respectively. In a preferred embodiment the pattern consists of alternating single modified and unmodified nucleotides.

40 **[0038]** In a further preferred embodiment of this aspect of the present invention the interfering ribonucleic acid subject comprises two strands, whereby a 2'-O-methyl modified nucleotide and a non-modified nucleotide, preferably a nucleotide which is not 2'-O-methyl modified, are incorporated on both strands in an alternate manner which means that every second nucleotide is a 2'-O-methyl modified and a non-modified nucleotide, respectively. This means that on the first strand one 2'-O-methyl modified nucleotide is followed by a non-modified nucleotide which in turn is followed by 2'-O-methyl modified nucleotide and so on. The same sequence of 2'-O-methyl modification and non-modification exists on the second strand, whereby there is preferably a phase shift such that the 2'-O-methyl modified nucleotide on the first strand base pairs with a non-modified nucleotide(s) on the second strand and vice versa. This particular arrangement, i. e. base pairing of 2'-O-methyl modified and non-modified nucleotide(s) on both strands is particularly preferred in case of short interfering ribonucleic acids, i. e. short base paired double-stranded ribonucleic acids because it is assumed, although the present inventors do not wish to be bound by that theory, that a certain repulsion exists between two base-pairing 2'-O-methyl modified nucleotides which would destabilise such duplex, preferably short duplexes. About the particular arrangement, it is preferred if the antisense strand starts with a 2'-O-methyl modified nucleotide at the 5' end

whereby consequently the second nucleotide is non-modified, the third, fifth, seventh and so on nucleotides are thus again 2'-O-methyl modified whereas the second, fourth, sixth, eighth and the like nucleotides are non-modified nucleotides. Again, not wishing to be bound by any theory, it seems that a particular importance may be ascribed to the second, and optionally fourth, sixth, eighth and/or similar position(s) at the 5' terminal end of the antisense strand which should not comprise any modification, whereas the most 5' terminal nucleotide, i. e. the first 5' terminal nucleotide of the antisense strand may exhibit such modification with any uneven positions such as first, optionally third, fifth and similar position(s) at the antisense strand may be modified. In further embodiments the modification and non-modification, respectively, of the modified and non-modified nucleotide(s), respectively, may be anyone as described herein.

[0039] Although not limited thereto, the double-stranded structure of the inventive ribonucleic acid, which is also referred to as duplex, is formed by the first strand and second strand, respectively, or the first and second stretch of contiguous nucleotides. The length of the first stretch and second stretch, respectively, is typically about 15 to about 23, preferably 17 to 21, and more preferably 18 or 19 bases. In connection with this it is to be noted that a length of less than 30 nucleotides, preferably less than 21 nucleotides does not cause any biological system which is basically capable of showing RNA interference and also interferon response, to develop an interferon response. The reason for this resides in the observation that a given cell is experiencing profound physiological changes when double-stranded RNA longer than 30 base pairs binds and activates the protein kinase PKR and 2',5'-oligoadenylate synthetase. Activated PKR stalls translation via phosphorylation of eIF2a, activated 2',5'-AS causes mRNA degradation. These effects are not desired in target validation and animal models because they overrule the effect of the target specific knockdown on the phenotype.

[0040] According to a sixth strategy in the design of interfering ribonucleic acids in accordance with claim 1 the ribonucleic acid comprises a double-stranded structure whereby the double-stranded structure comprises a first strand and a second strand, whereby the first strand comprises a first stretch of contiguous nucleotides and whereby said first stretch is at least partially complementary to a target nucleic acid, and the second strand comprises a second stretch of contiguous nucleotides whereby said second stretch is at least partially identical to a target nucleic acid whereby one terminus of the first strand and one terminus of the second strand are linked by a loop structure.

[0041] In an embodiment the loop structure is comprised of a non-nucleic acid polymer. Such non-nucleic acid polymer may be polyethylene glycol or similar polymers. The non-nucleic acid polymers may in principle be chosen, from the group comprising polymers which do not comprise a polynucleotide and allow that the two strands to be linked may actually hybridize to each other. To allow for such hybridization the molecule or moiety of the molecule linking the two stretches hybridizing with each other, has to have a certain molecular structure or molecular flexibility to allow the bending of the molecule so as to allow that both stretches get in close contact and in a three-dimensional orientation which permits hybridization. Such molecule or moiety factually acts as a hinge. In principle any molecule which complies with this requirement may be used in connection with the present invention. Besides polyethylene glycol amino acid based molecules may be used. Such amino acid based molecules may be either homopolymers or heteropolymers. A useful example is a homopolymer consisting of seven glycine residues which allows the generation of a hinge as required to bring the two stretches to hybridize in the close proximity as needed. This glycine based hinge is described, e. g., in Guan K. L. and Dixon J. E. (1991), Anal Biochem. 192, 262. In another embodiment the hinge may be formed by crown ethers known in the art.

[0042] In an alternative embodiment the loop is comprised of a nucleic acid. As used herein, LNA as described in Elayadi and Corey (2001) Curr Opin Investig Drugs. 2(4):558-61. Review; Orum and Wengel (2001) Curr Opin Mol Ther. 3(3):239-43; and PNA are regarded as nucleic acids and may also be used as loop forming polymers. Basically, the 5'-terminus of the first strand may be linked to the 3'-terminus of the second strand. As an alternative, the 3'-end of the first strand may be linked to the 5'-terminus of the second strand. The nucleotide sequence forming said loop structure is regarded as in general not being critical. However, the length of the nucleotide sequence forming such loop seems to be critical for sterical reasons. Accordingly, a minimum length of four nucleotides seems to be appropriate to form the required loop structure. In principle, the maximum number of nucleotides forming the hinge or the link between both stretches to be hybridized is not limited. However, the longer a polynucleotide is, the more likely secondary and tertiary structures are formed and thus the required orientation of the stretches affected. Preferably, a maximum number of nucleotides forming the hinge is about 12 nucleotides. It is within the disclosure of this application that any of the designs described above may be combined with the present sixth strategy, i. e. by linking the two strands covalently in a manner that back folding (loop) can occur through a loop structure or similar structure.

[0043] The present inventors have surprisingly found that if the loop is placed 3' of the antisense strand, i. e. the first strand of the ribonucleic acid(s) according to the present invention, the activities of this kind of RNAi are higher compared to the placement of the loop 5' of the antisense strand. Accordingly, the particular arrangement of the loop relative to the antisense strand and sense strand, i. e. the first strand and the second strand, respectively, is crucial and is thus in contrast to the understanding as expressed in the prior art where the orientation is said to be of no relevance. However, this seems not true given the experimental results presented herein. The understanding as expressed in the prior art is based on the assumption that any RNAi, is subject to a processing during which non-loop linked RNAi is generated. However, if this was the case, the clearly observed increased activity of those structures having the loop placed 3' of

the antisense could not be explained. Insofar a preferred arrangement in 5' → 3' direction of this kind of small interfering RNAi is second strand - loop - first strand. The respective constructs may be incorporated into suitable vector systems. Preferably the vector comprises a promoter for the expression of RNAi. Preferably the respective promoter is pol III and more preferably the promoters are the U6, H1, 7SK promoter as described in Good et al. (1997) *Gene Ther*, 4, 45-54.

[0044] Because of the general applicability of the concept of interfering RNA and thus the knockdown or knockout for a coding nucleotide such as an mRNA any gene producing such RNA may be modified in its expression by using any of the ribonucleic acid molecule according to the present invention. Because of this basic and generally applicable mechanism any application based thereon can be realised which imply the knockdown or knockout of a gene. A preferred application is the use of the inventive ribonucleic acid for target validation. As used herein, target validation shall mean a process that involves taking steps to prove that a DNA, RNA, or protein molecule is directly involved in a biological process, preferably in a process - causally - involved in a disease or non-standard condition and is therefore a suitable target for development of a new therapeutic compound. Sequence homology studies have successfully classified genes into target families. The enormous task of deciphering which of these targets are key players in diseases and which should be used for subsequent drug development needs to be addressed in an efficient manner. Therefore, the knockdown of gene expression should be reduced by 50-100%, preferably by 90% to see significant effects on the phenotype. In other cases depending on the gene, a knockdown of as little as 20% might be sufficient to yield a phenotype. A phenotype will be defined by comparison of cells containing functional RNAi molecules with cells containing non functional RNAi molecules. This will ensure a significant readout even under conditions where the protein function is inhibited only partially. Generally there is no linear correlation between the degree of mRNA reduction and the extent of the change in phenotype. It has to be acknowledged that for some proteins a reduction of about 20 % of the protein is sufficient to create a change in the phenotype whereas in case of other genes and mRNA, respectively, as little as 5 to 10 % remaining protein is sufficient to maintain the observed phenotype.

[0045] A further use of the ribonucleic acid molecules according to the present invention is its use for the manufacture of a medicament or its use as a medicament. Such medicament could either be used for the treatment and/or prevention of diseases or conditions such as any type of cancer where a gene and its product have been linked to the onset, cause or progression of this disease. Additionally, such medicament could be used to treat diseases where the presence or overexpression of a gene product is causing a pathological phenotype. In a preferred embodiment the disease is characterised by a gain of function and may be remedied through application or administration of the corresponding, biologically active RNAi. Diseases or conditions which may be treated by the medicament comprising a ribonucleic acid as disclosed herein, may be selected from the group comprising cancer, heart diseases, metabolic diseases, dermatological diseases, inflammatory diseases, immune system disorders and autoimmune disorders. The various forms of cancer include, but are not limited to, solid tumors and tumors of the hematopoietic system, such as glioblastoma, prostate cancer, breast cancer, lung cancer, liver cancer, pancreatic cancer and leukaemia. Metabolic diseases include, but are not limited to, obesity and diabetes. Dermatological diseases include, but are not limited to, psoriasis.

[0046] In another aspect the ribonucleic acid molecules according to the present invention may be used as diagnostics, preferably for those diseases as specified in connection with the above-mentioned diseases and conditions. Such diagnosis could be based on the observation that upon applying the ribonucleic acid molecules according to the present invention to a sample which preferably contains cells, a change in the expression pattern of the sample occurs. Preferably such sample comprises cells from a subject from whom it is assumed that it may exhibit said disease or condition to be treated or a predisposition thereto.

[0047] A further application of the nucleic acids according to the present invention resides in their use in the screening of pharmaceutically active compounds and/or lead optimization. The latter is done such as to monitor or determine the effect of candidate drugs such as small molecules and compare the effect created by said candidate drugs with the effect observed upon administering specific RNAi designed on the basis of the principles disclosed herein. In doing so candidate drugs having off-target effects may be eliminated from the screening process whereas those candidate drugs which create a similar or identical phenotype are deemed as highly relevant lead compound or may even be a pharmaceutically active compound themselves. In this approach, the highly specific RNAi molecules act as gold standard against which candidate drugs are measured.

[0048] In a further aspect the invention is related to a cell, preferably a knockdown cell, which contains a ribonucleic acid as disclosed herein. Such cell is preferably a cell which is either isolated or contained in a tissue or even organ which again preferably is not contained in an organism. However, the cell may also be contained in an organism. The cell is preferably a cell which is involved in the disease or condition which is to be treated by the inventive ribonucleic acids. This kind of knock-down cells may be used to generate an expression profile based on, e. g., mRNA or protein, in order to elucidate functional relationship and to determine downstream targets. In case the cell is a human cell, such human cell is an isolated human cell.

[0049] In a further aspect the invention is related to an organism containing a ribonucleic acid as disclosed herein. Preferably such organism is a vertebrate organism and more preferably the vertebrate organism is a mammal. A mammal as used herein is, among others and not limited thereto, an ape, a dog, a cat, a goat, a sheep, a pig, a guinea pig, a

rabbit, a mouse, and a rat. The organism is different from a human being.

[0050] In a still further aspect the present mention is related to a composition containing a ribonucleic acid according to the present invention. Preferably such composition comprises negative and positive controls either in combination with the effective ribonucleic acid or separated therefrom. Such composition may further comprise a solvent, preferably a buffer.

[0051] In a further aspect the present invention is related to a pharmaceutical composition containing a ribonucleic acid according to the present invention and a pharmaceutically acceptable carrier. Pharmaceutically acceptable carriers are known to the one skilled in the art and comprise, among others, diluent, buffers and the like. The pharmaceutical composition may compose further pharmaceutically active compounds. In case the disease or condition to be treated using the ribonucleic acid molecules according to the present invention are preferably those which are already now used in connection with the treatment of said diseases or conditions. Due to the different mode of action of the ribonucleic acid molecules according to the present invention and the medicaments used for the treatment of said diseases and conditions according to the prior art, synergistic effects will happen.

[0052] The invention is now further illustrated by reference to the figures and examples from which further features, embodiments and advantages of the present invention may be taken.

Fig. 1 shows a schematic illustration defining the terminology as used herein. The upper of the two strand is the first strand and the antisense strand of the targeted nucleic acid such as mRNA. The second strand is the one which essentially corresponds in its sequence to the targeted nucleic acid and thus forms the sense strand. Both, the first strand and second strand form a double-stranded structure, typically through Watson Crick base pairing.

Fig. 2 illustrates some embodiments of the ribonucleic acid molecules of the present invention with patterns of modified and unmodified groups of nucleotides which is also referred to herein as pattern of modification. The modified groups of nucleotides are also referred to herein as group of modified nucleotides. The unmodified nucleotides or unmodified groups of nucleotides referred to as flanking group(s) of nucleotides herein, as used herein may also have one or several of the modification(s) as disclosed herein which, however, is/are different from the modification of the nucleotides forming the group(s) of modified nucleotides. In Fig. 2A the modified and unmodified groups of nucleotides, i. e. the groups of modified nucleotides and the flanking groups of nucleotides on both the first stretch and the second stretch are located on corresponding parts of the stretches and are thus aligned to each other (groups of modified nucleotides on the first strand aligned with groups of modified nucleotides on the second strand and flanking groups of nucleotides on the first strand aligned with flanking group of nucleotides on the second strand), whereas in Fig. 2B the pattern realised on the first strand is also realised on the second strand, however, with a phase shift such that the modified group of nucleotides of the first stretch is base pairing with an unmodified group of nucleotides of the second stretch and vice versa so that a group of modified nucleotides on the first strand alignes with a flanking group of nucleotides on the second strand. In Fig. 2C a further possibility of arranging the modified and unmodified groups of nucleotides is realised. It is also within the present invention that the pattern of the first stretch is independent from the pattern of the second stretch and that both patterns partially overlap in terms of relative position to each other in the double-stranded structure defined by base pairing. In a further embodiment the extent of this overlapping can vary over the length of the stretch(es) and strand(s), respectively.

Fig. 3 shows the result of a knockdown experiment using RNAi molecules with different end protection groups. More particularly Fig. 3A shows that the various forms of end protected RNAi molecules are functional on the knockdown of PTEN mRNA.

Fig. 3B shows the sequence of the different RNAi molecules used in the experiment the result of which is depicted in Fig. 3A. Fig. 3C shows the result of an immunoblot analysis of PTEN protein after treatment with modified RNAi molecules in comparison to PTEN specific antisense constructs.

Fig. 4 shows that the 3' overhang of RNAi molecules is not important for RNA interference. More particularly, Fig. 4A shows a dose response curve of different RNAi molecules and Fig. 4B shows the sequence of the RNAi molecules used in the experiment the result of which is shown in Fig. 4A.

Fig. 5 shows that duplex length of the RNAi molecules has to be at least 18-19 nucleotide. More particularly, Fig. 5B shows the sequence of the PTEN specific RNAi molecules used in the experiment the result of which is depicted in Fig. 5A as dose response curve.

Fig. 6 shows that four terminal mismatched nucleotides in RNAi molecules with a length of 19 nucleotides are still functional in mediating Akt1 knockdown. More particularly, Fig. 6B shows the sequence of the RNAi molecules used

in the experiment the result of which is depicted in Fig. 6A.

Fig. 7 shows further results on duplex length requirements and tolerance for mutation in siRNAs. More particularly, Fig. 7A shows the various constructs used (left panel) and the respective impact on inhibition of Akt1 mRNA expression in HeLa cells relative to the expression of p110 α used in the indicated amounts of siRNA molecules (right panel). The nucleotide changes in the mismatch siRNA molecules are indicated by arrows; the 3' desoxynucleotide, if any, are indicated in capital letter. Fig. 7B shows the various PTEN specific siRNAs (left panel), the inhibition of PTEN mRNA expression in HeLa cells expressed as ratio PTEN/p110 α , at various amounts of siRNA (middle panel) and Fig. 7C a Western Blot analysis depicting the inhibition of PTEN protein expression using PTEN specific siRNA (30nM) and respective mismatch siRNA after 48 and 96 hours, respectively, with p100 α being used as loading control.

Fig. 8 shows the result of studies on the stability in serum conferred to RNAi molecules by 2'-O-methylation and that end modifications have no beneficial effects on RNAi stability. More particularly, Fig. 8A shows the result of a gel electrophoresis of the various RNAi molecules depicted in Fig. 8B being subject to incubation with fetal calf serum.

Fig. 9 shows that an amino end modification results in loss of activity. Fig. 9B shows the particular RNAi molecules used in the experiments the result of which is shown in Fig. 9A expressed as PTEN/p 110 α expression level ratio. Fig. 9C shows the design principles which may be deduced from the results depicted in Fig. 9A. As used in Fig. 9C the term functional means functionally active in the particular assay system as described in the example and "not functional" means not functionally active in said system.

Fig. 10 shows that 2'-O-Alkyl (methyl) modifications stabilize RNAi molecules but also result in reduction of their activity. More particularly, Fig. 10C shows the sequence of the RNAi molecules used in the experiment the result of which is depicted as a dose response curve in Fig. 10A. Fig. 10B shows the result of a gel electrophoresis of the various RNAi molecules depicted in Fig. 10C being subject to a two hour incubation in fetal calf serum.

Fig. 11 shows the result of an experiment on the efficacy of RNAi molecules with blocks of 2'-O-methyl modifications with Fig. 11A graphically depicting the results of said experiments as a dose response curve and with Fig. 11C showing the sequences of the particular RNAi molecules used in said experiments, Fig. 11B shows the result of a gel electrophoresis of the various RNAi molecules depicted in Fig. 11C being subject to a two hour incubation in fetal calf serum.

Fig. 12 shows that alternating 2'-O-methyl modification result in activity of the modified RNAi molecules compared to unmodified forms. More particularly, Fig. 12B shows the sequence of the RNAi molecules used in this experiment the result of which is depicted in Fig. 12A. Fig. 12C shows the stability of said RNAi molecules following incubation in serum for two hours, whereas Fig. 12D shows an immunoblot for PTEN protein upon application of different RNAi molecules to HeLa cells. As may be taken therefrom RNAi molecules with alternating modifications are stabilized against endonuclease degradation and active in mediating a PTEN protein knock down.

Fig. 13 shows the result of a Western Blot analysis to determine the time course of PTEN protein knock down. Cells were continuously transfected with 2'-O-Methyl modified versus unmodified RNAi molecules using cationic lipids for 72 h. Protein lysates were prepared and analysed by immunoblot after 48 and 120 h. For the 96 h and 120 h timepoints the cells were splitted, replated and incubated in the absence of RNAi molecules for additional 24 and 48 h..

Fig. 14 shows a Western Blot depicting the protein knock down of PTEN being persistent using alternating modified RNAi molecules versus unmodified RNAi molecules. Transfection were performed for only 5 h and new medium without transfection reagents was added. Lysates were analysed by immunoblot 72h and 96h post transfection with the indicated RNAi molecules.

Fig. 15 shows that siRNA molecules with distinct 2'-O-methyl ribonucleotides modifications show increased stability in serum and mediate protein knock-down in HeLa cells. More particularly, Fig. 15A indicates the various siRNA molecule constructs used (left panel), whereby 2'-O-methyl ribonucleotides modifications are underlined and indicated by bold letters in the sequence. Inhibition of PTEN mRNA expression in HeLa cells transfected with the indicated amounts of modified siRNA molecules is expressed as ratio PTEN/p110 α and indicated on the right panel. Fig. 15B shows on the left panel the various siRNA constructs used and on the right panel a PAA gel electrophoresis of modified and unmodified siRNA molecules after incubation in serum; the various constructs with 2'-O-methyl ribonucleotides are indicated by underlining and bold printing. Fig. 15C shows an SDS-PAGE based immunoblot illustrating the inhibition of PTEN protein expression using various of the siRNA constructs (30 nM) as depicted in

Fig. 15A and 15B, respectively. Again, p110 α is used as loading control. Finally, Fig. 15D is an immunoblot indicating a prolonged protein knock-down, i. e. the inhibition of PTEN protein expression, upon administration of siRNA molecules (30 nM) with distinct 2'-O-methylribonucleotides modifications after 48 and 128 hours. As in Fig. 15C, p 110 α is used as loading control.

Fig. 16 shows that siRNA molecules with distinct 2'-O-methylribonucleotides modifications which are specific for Akt1 and p110 β mRNA show increased stability in serum and mediate protein knock-down in HeLa cells. More particularly, Fig. 16A indicates on the left panel the various constructs used whereby again 2'-O-methylribonucleotides are underlined and printed in bold. The integrity of the indicated siRNA molecules after incubation in serum is shown in the right panel. Fig. 16B shows an immunoblot of Akt1, Akt2 and Akt phosphorylation and p110 being used as a loading control upon transfection of the cells with the indicated siRNAs (30 mM). Fig. 16C shows various p 110 β specific siRNA constructs (left panel) with the 2'-O-methyl modifications being underlined and printed in bold, and the result of an immunoblot analysis (right panel) of the inhibition of the phosphorylation of the downstream kinase Akt1 by said siRNA constructs. p110 α has been used as a loading control.

Fig. 17 shows the efficacy of various RNAi molecules with hairpin structures as dose response curve while Fig. 17B shows the structure of said RNAi molecules the result of which is depicted in Fig. 17A. Synthetic siRNAs with different loops are functional in reducing the p110 β , Akt1 and Akt 2 expression. (14A) Inhibition of p110 β mRNA expression in siRNA transfected HeLa cells. Samples were analyzed in parallel for the level of p110 β mRNA expression 24h after transfection of the indicated siRNAs. The transfected bimolecular siRNAs (21mer with 3' TT overhangs, molecule 1AB) or the monomolecular siRNAs with loop structures are schematically shown. Note that the position of the loops (HIV derived pA-loop; (A)₁₂-loop) relative to the antisense sequence is reversed in 3A, 4A relative to 3B, 4B. The 2AB siRNA molecule contains 6 mismatches in the 21mer duplex and serves as a negative control together with the untreated sample. RNA was prepared und subjected to real time RT-PCR (Taqman) analysis. p110 β mRNA levels are shown relative to the mRNA levels of p110 α , which serve as an internal reference. Each bar represents triplicate transfections (\pm standard deviation). HeLa cells were transfected at 50% confluence (2500 cells per 96 well) with siRNAs at the indicated concentrations in growth medium.

Fig. 18 shows the efficacy of various RNAi molecules with intermolecular and intramolecular loop structures as dose response curves. (18A) Inhibition of Akt1 mRNA expression in siRNA transfected HeLa cells. Samples were analysed in parallel for the level of Akt1 and Akt2 mRNA expression 24h after transfection of the indicated siRNAs. The different loops (A-loops; GAGA-loop and a polyethylenglycol (PEG)-linker) and their putative secondary structure are shown schematically. The siRNA molecule 9A is specific for Akt2 and serves as a negative control. Note that 10A and 10B do not contain self-complementary sequences and are transfected in combination. Akt1 mRNA levels is shown relative to the mRNA levels of p110 β , which served as internal control. (18B) Inhibition of Akt2 mRNA expression in HeLa cells transfected with the indicated siRNA molecules. Akt2 mRNA levels is shown relative to the mRNA levels of p110 β . The Akt1 specific molecule 7A serves here as a negative control.

Fig. 18 C shows a Western Blot analysis on Akt protein depicting the functionality of synthetic siRNAs with different loops in specifically reducing the Akt1 and Akt 2 expression. Inhibition of Akt1 and Akt2 protein expression were analysed by immunoblot. The cells were harvested 48h after transfection of the indicated hairpin siRNAs (20nM). Cell extracts were separated by SDS-PAGE and analysed by immunoblotting using anti-p110 antibody, anti Akt 1/2. Similar results were obtained with an antibody specific for the phosphorylated form of Akt1. The positions of p110 α , another catalytic subunit of PI 3-kinase, which was used as a loading control, and of Akt1, Akt2 and phosphorylated Akt (P*-Akt) are indicated on the left.

Fig. 19 shows an NH₂ modification, also referred to herein as amino modification, which may be present at either the 3'-OH terminal nucleotide or the 5' terminal nucleotide. The amino group is attached to the phosphate which in turn is attached to the OH group of the sugar moiety, through an alkyl group comprising an alkyl chain of 1 to 8, preferably 6 C atoms, whereby the second C atom close to the phosphate group has a CH₂OH group attached thereto. As an alternative the linker may be formed by an ether whereby the ether is comprised of two alcohols whereby one alcohol is an amino alcohol and the other is a dialcohol with one alcohol group involved in the formation of the ether group and the other one being an OH group located at either of the C atoms, preferably at the second C atom relative to the phosphate group.

Example 1: Dose response of synthetic duplex RNAi molecules

[0053] In this example the impact of NH₂ end protection groups on the activity of duplex RNAi molecules was inves-

tigated. Synthetic siRNAs were purchased from Biospring (Frankfurt, Germany). The ribo-oligonucleotides were resuspended in RNase free TE to a final concentration of 50 μ M. In the case of bimolecular siRNA molecules equal aliquots (100 μ M) were combined to a final concentration of 50 μ M. For the formation of intramolecular duplexes the siRNAs were incubated at 50 °C for 2 min in annealing buffer (25mM NaCl; 5mM MgCl₂) and were cooled down to RT. Transfections were carried out in 96 well or 10-cm plates (at 30% to 50% confluence) by using various cationic lipids such as Oligofectamine, Lipofectamine (Life Technologies), NC388 (Ribozyme Pharmaceuticals, Inc., Boulder, CO), or FuGene 6 (Roche) according to the manufacturer's instructions. RNAi molecules were transfected by adding pre-formed 5x concentrated complex of annealed RNAi and lipid in serum-free medium to cells in complete medium. Prior to transfection 2500 HeLa cells were plated per well 15 - 18 hours before transfection for the 96 well format.

[0054] The total transfection volume was 100 μ l for cells plated in 96-wells and 10 ml for cells in 10 cm plates. The final lipid concentration was 0.8 to 1.2 μ g/ml depending on cell density; the RNAi concentration is indicated in each experiment.

[0055] Complex formation was allowed to take place for 30 min at 37°C. Complexes were added to cells to yield a final 1x concentration of both lipid and RNAi. Depending on the analysis performed following transfection, cells were lysed using a standard cell lysis buffer for protein extraction (Klippel, A., Escobedo, J. A., Hirano, M. and Williams, L. T. (1994). Mol Cell Biol 14, 2675-2685) or a denaturing buffer for RNA isolation according to the RNA isolation kit (Invitek, Berlin (Germany) 24 to 48 hours post transfection for RNA analysis and 48 to 72 hours post transfection for protein analysis by Western Blot.

20 Determination of the relative amounts of RNA levels by Taqman analysis:

[0056] 24h post transfection the RNA of cells transfected in 96-wells was isolated and purified using the Invisorb RNA HTS 96 kit (InVitek GmbH, Berlin). Inhibition of PTEN mRNA expression was detected by real time RT-PCR (Taqman) analysis using 300 nM PTEN 5' primer CACCGCCAAATTAACTGCAGA, 300 nM PTEN 3' primer AAGGGTTTGA-TAAGTTCTAGCTGT and 100 nM of the PTEN Taqman probe Fam-TGCACAGTATCCTTTGAAGACCATAACCCA-Tamra in combination with 40 nM β -actin 5' primer GTTTGAGACCTTCAACACCCCA, 40 nM β -actin 3' primer GACCA-GAGGCATACAGGGACA and 100 nM of the β -actin Taqman probe Vic-CCATGTACGTAGCCATCCAGGCTGTG-Tamra. The Akt primers and probes are determined in Sternberger et al. (Sternberger, a.a.O.) and are used according to the manufacturer's instructions (Applied Biosystem; use of Amplicon Set). Also said primers and probes may be designed using the software program Primer Express (Applied Biosystem). The reaction was carried out in 50 μ l and assayed on the ABI PRISM 7700 Sequence detector (Applied Biosystems) according to the manufacturer's instructions under the following conditions: 48°C for 30 min, 95°C for 10 min, followed by 40 cycles of 15 sec at 95°C and 1 min at 60°C.

[0057] RNA knockdown is shown by real time RT-PCR analysis of HeLa cells transfected with 21 nt long siRNA duplex molecules unmodified and modified with either NH₂ or inverted Abasics groups at the 5'-end at a lipid carrier concentration of 1.0 μ g/ml. Cell density was 2000 cells/well. Modifications on the 3'-end are either RNA overhangs, RNA overhangs with amino groups or DNA overhangs.

[0058] **Preparation of cell extracts and immunoblotting.** Cells were washed twice with cold phosphate-buffered saline and lysed at 4°C in lysis buffer containing 20 mM Tris (pH 7.5), 137 mM NaCl, 15% (vol/vol) glycerol, 1% (vol/vol) Nonidet P-40 (NP-40), 2 mM phenylmethylsulfonyl fluoride, 10 mg aprotinin per ml, 20 mM leupeptin, 2 mM benzamidine, 1 mM sodium vanadate, 25 mM β -glycerol phosphate, 50 mM NaF and 10 mM NaPPI. Lysates were cleared by centrifugation at 14,000 x g for 5 minutes and aliquots of the cell extracts containing equal amounts of protein were analyzed for protein expression by Western-blotting: Samples were separated by SDS-PAGE and transferred to nitrocellulose-filters (Schleicher & Schuell). Filters were blocked in TBST buffer (10 mM Tris-HCl (pH 7.5), 150 mM NaCl, 0.05% (vol/vol) Tween 20, 0.5% (wt/vol) sodium azide) containing 5% (wt/vol) dried milk. The respective antibodies were added in TBST at appropriate dilutions. Bound antibody was detected using anti-mouse- or anti-rabbit-conjugated horse radish peroxidase (Transduction Laboratories) in TBST, washed, and developed using the SuperSignal West Dura (Pierce) or ECL (Amersham) chemoluminescence substrates (c.f. Sternberger et al. (2002). *Antisense. Nucl. Ac. Drug Dev. in press.*

[0059] **Antibodies.** The murine monoclonal anti-p110 antibody U3A and the murine monoclonal anti-p85 antibody N7B have been described (Klippel et al., 1994, aaO). Rabbit polyclonal anti-Akt and anti-phospho Akt (S473) antibodies were obtained from Cell Signaling Technology. The murine monoclonal anti-PTEN antibody was from Santa Cruz Biotechnology. The PTEN 53 specific antisense molecule, i. e. geneBloc, is described in Sternberg et al. [Sternberger, supra] having the following sequence (ucuccuTTGTTCTGcuaacga), whereby the nucleotide depicted in lower case are ribonucleotides whereas the nucleotide in capital letters are desoxyribonucleotides. This antisense molecule is also identical to RNAi 1A without TT.

[0060] The results are shown in Fig. 3A and the respective RNAi molecules in Fig. 3B which are directed to the mRNA of PTEN. The nucleotides written in lower case letters represent ribonucleotides whereas capital letters represent desoxyribonucleotides. The term NH₂ indicates that the 3' -position of the ribonucleotide was modified by an amino group. The RNAi molecules used in this and other examples disclosed herein are also referred to as small interfering RNA

molecules siRNA. It is to be noted that in any of the figures contained herein the upper strand is the antisense or first strand, whereas the lower strand is the sense or second strand of the interfering RNA molecule.

[0061] As can be taken from Fig. 3A amino end modifications such as amino modification and inverted abasics modification of the terminal OH group of the nucleic acid are as potent as unmodified ends when the modification is located 5 at the 3' end of the antisense strand (see also Fig. 8A; 8B). Therefore chemical modification to stabilize or with other beneficial properties (delivery) will be tolerated without activity loss when located at the 3' OH; especially when the 3'OH is located on an overhanging nucleotide.

[0062] For the experiment shown in Fig. 3C similar conditions as outlined above were used. The first strand and the second strand of the RNAi were either modified by a NH₂ group at the 3'-position of the ribose moiety or by an inverted abasic at said positions. The first construct is designated as siRNA-NH₂ (3A3B) the second as siRNA-iB (4A4B). The sequence of both molecules is depicted in Fig. 3B. The term 3A3B indicates that the interfering ribonucleic acid consists of strand 3A as the antisense strand and strand 3B as the sense strand. For reason of comparison an antisense oligonucleotide designated GB53 (Steinberger et al., *supra*) was generated which was directed against the PTEN mRNA as well. The particularities of this latter experiment were as follows.

[0063] As may be taken from Fig. 3C end protected RNAi molecules depicted in Fig. 3B are functional in yielding a 10 PTEN protein knockdown.

[0064] From this example it can be taken that both end protection groups render RNAi molecules active in knocking 20 down PTEN protein. This inhibition is as efficient as inhibition with antisense constructs but at lower concentrations used which is a clear advantage over the already very powerful antisense technology.

Example 2: Overhang requirements for RNAi duplex activity in vivo

[0065] The experimental procedures were the same as depicted in connection with example 1 except that the PTEN 25 mRNA targeting interfering RNAi molecules were differently designed. The results are shown in Fig. 4A as dose response curves with Fig. 4B showing the particular sequence and modifications of the interfering RNAi molecules used to generate the data depicted in Fig. 4A. The nomenclature is such that, e. g., RNAi 18 is composed of strand 18A as antisense strand and strand 18B as sense strand.

[0066] Blunt ended molecules are compared to molecules with 3'-overhangs (RNAi 18) and 5'-overhangs (RNAi 30 30 and RNAi 31) in their activity to knockdown PTEN mRNA in HeLa cells. The activity of blunt ended molecules (RNAi 28) and molecules with 5'-overhangs is comparable to the activity of molecules with 3'-overhangs. This shows that 3'-overhangs are not essential for RNAi activity.

Example 3: Duplex length requirements of interfering RNA molecules for RNAi activity in vivo

[0067] The experimental approach was similar to the one outlined in connection with example 1 except that the interfering RNA molecules were directed against the mRNA of Akt1. The negative control to show the specificity of the RNAi molecules was again p110 mRNA. The experimental results are shown in Fig. 5A with the particularities of the interfering RNAi molecules used being represented in Fig. 5B. Similar experiments were carried out with further siRNA 40 constructs which are depicted in Fig. 7A, left panel, whereby the arrows indicate mismatches and desoxyribonucleotides are expressed in capital letters. The inhibition of Akt1 mRNA expression in HeLa cells transfected with the indicated amounts of siRNA molecules is depicted on the right panel of Fig. 7A.

[0068] Taqman analysis on Akt RNA from HeLa cells transfected with different RNAi molecules shows that the doublestrand duplex of the siRNA molecules has to be longer than 17 base pairs to show activity whereas molecules with 45 17 base pair long duplexes or shorter are not functional even if sequence-specific overhangs are added. The shortest RNAi molecules successfully tested were 18 to 19 nucleotides or base pairs in length. It is to be noted that the design of the interfering RNA molecule 51A/51B referred to as RNAi 51 corresponds to the one as described in international patent application WO 01/75164. The RNAi molecule 55A/55B comprises a stretch of 17 nucleotides and has a clearly decreased activity in terms of degradation of Akt1 mRNA.

[0069] As may be taken from Fig. 7A 19 nt long duplexes are highly efficient in reducing Akt1 mRNA levels independent 50 of the nature (desoxy- or ribonucleotides) of the 3' overhang (compare molecules 1AB, 2AB, 3AB, 4AB). The 17 nucleotide long siRNA (molecule 5AB) showed a dramatically reduced silencing activity confirming the above expressed understanding that active siRNA duplexes should be at least 18 nt or longer. Without being wished to be bound by any theory this result may be explained mechanistically by two different requirements. First, a minimum base pairing of 18 nt between the antisense of the siRNA and the target mRNA may be obligatory, or second, incorporation into the RNA-induced silencing complex (RISC) requires a minimum length of the siRNA duplex. To address this question a 19 nt long siRNA 55 duplex molecule with one and two terminal mutations (CG and UA inversion) relative to the wildtype sequence was synthesised (molecules 6AB and 7AB). Both molecules, even the molecule with a stretch of only 15 nt base pairing to the target mRNA were functional in inducing the Akt1 mRNA level. Therefore, it can be concluded that the duplex length

itself, but not the base pairing of the antisense siRNA with the target mRNA seems to determine the minimum length of functional siRNAs. This suggests that the length of the double-stranded helix is an important determinant for the incorporation into the RISC complex. The introduced mismatches at the terminal ends of the siRNA duplexes had little effect on RNA interference.

5 [0070] Given the experimental results, the minimum requirement for optimum RNAi mediated interference is thus a duplex length of 18 or 19 nucleotides, independent of the further design of the RNAi molecules such as blunt end or 5'-overhang or any other form as disclosed herein, but generally applicable to RNAi molecules. However, it has to be acknowledged that the particular design of the RNAi molecules may confer further advantages to said molecules, such as, e. g., increased efficiency and increased stability, respectively.

10 **Example 4: Target -antisense homology requirements for RNAi in vivo**

[0071] The experimental set-up was similar to the one described in example 1, whereby the RNAi is specific for Akt1. In addition, a PTEN specific interfering RNA molecule was designed and used as negative control. The results are shown 15 in Fig. 6A and Fig. 6B. Basically the same experiment was carried out using further siRNA molecules as depicted in Fig. 7B with the results being indicated in Fig. 7B (right panel) and Fig. 7C, respectively.

[0072] Having established the minimal duplex length of 18 or more than 18 nucleotides for functional siRNA molecules 20 we have asked the question how many matching nucleotides between target mRNA and siRNA are necessary for silencing activity. As shown by Taqman analysis on Akt1 RNA a stretch of 19 to 15 nucleotides perfectly matching to the target RNA, in the present case Akt 1, is sufficient to mediate RNAi activity. A PTEN specific RNAi molecule does not 25 reduce RNA amounts of Akt1 thus confirming the specificity of this approach. Mismatches of one or two nucleotides at any or both ends of a strand are functional suggesting that a homolog stretch of 15 nt between a target mRNA and RNAi is sufficient for gene silencing. It can be concluded from these data that unspecific gene silencing can occur by chance 30 through unspecific binding to unrelated targets. This is based on the understanding that a stretch of 15 to 17 matching base pairs is not specific for a single gene and will occur by chance considering the complexity and size of the genome 35 or transcriptosome of vertebrates. Apart from the afore-described experiments also the location of the mismatch was subsequently analysed. For this purpose a 19 nt long blunt siRNA directed against PTEN mRNA was used. The sequence changes in one siRNA strand were compensated by complementary changes in the other strand to avoid disrupting duplex formation. As may be taken from both Figs. 7B and C, respectively, a siRNA with only one point mutation in the centre of the molecule was severely compromised in its ability to use mRNA and protein expression levels. This result indicates that the RNA machinery is highly discriminative between perfect and imperfect base pairing between target mRNA and siRNA in the centre of the duplex. This extreme dependence on a perfect complementarity between target and siRNA has already been described for RNAi interference in the Drosophila system, however, not yet in connection with mammalian systems such as HeLa.

[0073] Based on this observation the present invention is reducing this off-target problem of siRNA by two approaches. First by reducing the molecule length of the siRNA molecules to the minimal requirements (18-19 nt) and thereby reducing the chance of homology to off-targets. Second, by inactivation of the sense strand to prevent an unwanted RNA silencing caused by accidental complementarity of the sense strand to an unrelated target RNA (see also Example 6).

40 **Example 5: Stability of modified RNAi molecules in serum**

[0074] Oligonucleotides were incubated in human serum for 15 min and two hours and loaded on 10% polyacrylamide gel with untreated controls. The results are shown in Fig. 8A. The various RNAi molecules used are shown and described in more detail in Fig. 8B.

[0075] From this example it can be taken that the RNAi duplex of RNA molecules with all nucleotides modified with 45 2'-O-methyl groups (RNAi molecules 79A79B and 28A28B) have higher stability in serum. It is also shown that a blunt duplex is more stable than the duplex molecule with overhangs. From this the conclusion may be drawn that end protection (e.g. iB or Amino) is not increasing the stability in serum.

[0076] In addition, it can also be concluded that in contrast to the understanding in the art before the filing of this 50 application endonucleases rather than exonucleases are more important in the protection of RNAi molecules.

[0077] In view of this, in addition to the various modifications or designs of the inventive RNAi molecules as disclosed in this application a further or additional modification of the nucleotides may be the use of a phosphorothioate backbone 55 of the RNAi molecules which may be either complete or partial in order to inhibit endonuclease function. A complete phosphorothioate backbone means that any of the nucleotides exhibits a phosphorothioate group whereas a partial phosphorothioate backbone means that not all of the nucleotides forming the RNAi molecule have a phosphorothioate modification. This modification is suitable to increase the lifetime of RNAi molecules irrespective of the further design of RNAi molecules. In this regard, a partially or completely phosphorothioate modified RNAi is subject to the present invention which may be realized in connection with the different strategies for the design of interfering RNA molecules

as disclosed herein or with any of the designs known in the art.

Example 6: Inactivation of the sense strand by NH₂ end protection groups on the 5' and 3' ends

5 [0078] The experimental set-up was similar to the one described in connection with example 1 with the target nucleic acid sequence being PTEN mRNA. The concentration of HeLa cells was 2,000 cells per well. RNA of PTEN was analysed in Taqman assays after transfection of differently modified RNAi molecules. The different interfering RNA molecules used are depicted in Fig. 9B whereas the experimental results are shown in Fig. 9A.

10 [0079] As may be taken from the dose response curves of various RNAi molecules depicted in Fig. 8A RNAi molecules are functional when the sense strand, i. e. the second strand, is modified on both ends with amino groups. Particularly effective are RNAi molecules 20A26B, 18A26B, and 28A26B. The lowest activity is shown by RNAi molecule 26A26B which corresponds to end modification on all 4 ends of the duplex (Tuschl is 18AB).

15 [0080] However, RNAi activity is also achieved when the antisense strand, i. e. the first strand, is modified only at the 3' end leaving a free OH group at the 5' end (RNAi constructs 22A26B; 20A26B). There is no activity when the antisense strand is modified with amino groups on both the 5' and the 3' end (26A26B). This leads to the conclusion that any end of the antisense strand and more particularly the 5' end of the antisense should be kept without modifications. Additionally, it is worth stating that the NH₂ end modification can be used to inactivate the sense strand on the 5' and 3' end and therefore reduce off-target effects mediated by an otherwise functional sense strand which results in a significantly increased specificity of the RNAi molecule which is advantageous for target validation as well as for any medical use of the RNAi molecule.

20 [0081] The further generalisation of the results from this experiment is depicted in Fig. 9C. Functionally active RNAi are accordingly those not having an amino modification at the antisense strand or having an amino modification only at the 3' end of the antisense strand whereas an amino modification at both ends of the antisense strand is not functional, i. e. does not result in a knockdown of the target mRNA.

25 **Example 7: Impact of 2'-O-methyl modification of RNAi molecules for endonuclease protection.**

30 [0082] RNA knockdown is again shown using the real time RT-PCR analysis on HeLa cells transfected with RNAi duplex molecules directed against the PTEN mRNA as represented in Fig. 10A. Experimental procedures were basically the same as specified in example 1. The structure of the RNAi molecules investigated and their dose responses, which are depicted in Fig. 10A, are shown in Fig. 10C. The nucleotides printed in bold are those having a 2'-O-methyl modification.

35 [0083] It is illustrated by the dose response curves shown for various RNAi molecules in Fig. 10A that internal 2'-O-alkyl groups are reducing RNAi activity. Preferably such 2'-O-alkyl groups are 2'-O-methyl or 2'-O-ethyl groups. However, molecules with unmodified nucleotides in combination with 2'-O-alkyl modification show significant activity. As is also depicted in Fig. 10A there is no activity when the antisense strand is all modified with 2'-O-methyl groups and the sense strand is not modified (c. f., e. g., RNAi molecule 79A28B). Taken the results of a stability test such as incubation of the various RNAi molecules in serum, as depicted in Fig. 10B, shows that 2'-O-alkyl modifications stabilize RNAi molecules against degradation. This clearly beneficial effect, however, is at least to a certain degree counterbalanced by the effect that 2'-O-alkyl modifications generally result in a reduced knockdown activity. Accordingly, the design of RNAi molecules has to balance stability against activity which makes it important to be aware of the various design principles as disclosed in the present application.

45 **Example 8: Impact of blocks of internal 2'-O-methyl modifications on the stability of RNAi molecules in serum.**

50 [0084] The experimental approach in connection with this study was actually the same as depicted in example 1. Again, PTEN RNA is analysed by real time RT-PCR on HeLa cells at a density of 2000 cells/well which were transfected with different doses of RNAi molecules. RNAi molecules were incubated in serum for two hours and analysed on a 10% polyacrylamide gel. The results of this study are illustrated in Figs. 11A to 11C, whereby Fig. 11A shows the dose response of the various RNAi molecules depicted in Fig. 11C and Fig. 11B shows the result of a stability test using some of the RNAi molecules depicted in Fig. 11C. It is to be acknowledged that the nucleotides written in bold in Fig. 11C are the ones carrying a modification which is in the present case of a 2'-O-methyl modification of the ribose moiety of the nucleotides.

55 [0085] There is a dose dependent inhibition by the unmodified RNAi molecules. It is also shown that the 2'-O-methyl modification of the core 9 nucleotides makes the RNAi stable in serum and allows activity of the duplex in the meaning of mediating the interference phenomenon leading to a degradation of the PTEN mRNA. Total modification of the sense strand makes the RNAi molecule stable in serum and allows certain activity.

[0086] Alternating blocks of 5 nucleotides with 2'-O-methyl modification renders the RNAi molecule stable in serum

and allows activity on PTEN RNA as shown by incubating the RNAi duplex in serum for two hours and loading the samples on a 10% polyacrylamide gel. As may be taken from Fig. 11B the duplex comprising strands 80A and 80B is strongly degraded after incubation in serum for two hours. The duplex consisting of strands 82A and 82B confirms the result that the 5'-end of the first strand which comprises the antisense strand should not be modified at the 5'-terminal nucleotides (compare 82A82B with the reverse orientated 81A81B). This is also confirmed by the results obtained having the duplex consisting of the strands 86A and 86B which is both active and stabilised in serum. It is noteworthy that molecules with unmodified blocks at the terminal 5' of the antisense strand are more active whereby the 5' terminal OH group is preferably not derivatized.

[0087] Further experiments were carried out using different modification patterns of 2'-O-methyl modification of the nucleotides. The results thereof are shown in Fig. 12A to 12C and further discussed herein in example 9.

Example 9: The impact of alternating internal 2'-O-alkyl modification on serum stability of RNAi molecules.

[0088] The experimental set-up for performing this kind of study was the same as used in connection with the studies reported in example 1 and example 8, respectively, with the targeted nucleic acid being again PTEN mRNA. HeLa cells were transfected with the different RNAi molecules depicted in Fig. 12B and RNA knockdown was demonstrated using real time RT-PCR on PTEN RNA in a dose-dependent manner (Fig. 12A). The stability of the various RNAi molecules after 15 min and two hours in serum at 37 °C is depicted in Fig. 12C and a Western Blot for p110 and PTEN as the target-protein of the various RNAi molecules is depicted in Fig. 12D with the RNAi molecules tested being the same in both the experiments underlying Fig. 12C and Fig. 12D.

[0089] As illustrated in Fig. 12A and Fig. 12C nucleotides modified with 2'-O-methyl groups alternating with unmodified nucleotides render RNAi molecules stable in serum while still allowing them to be active in the sense of interfering with the target mRNA. It is shown that incubation of RNAi duplex molecules for 15 min and two hours in serum will degrade the unmodified duplex and the duplex where the 10 most 5'-positioned nucleotides are unmodified.

[0090] In the RNAi molecules represented in Fig. 12B various patterns of modified and unmodified nucleotides are realised. The RNAi molecule 94A1/94B1 comprises a structure wherein a modified nucleotide is flanked by an unmodified nucleotide with the unmodified nucleotide being located at the 5' end of the first strand. The RNAi molecule comprised of strands 94A2 and 94B2 is another example where the modified nucleotides and the unmodified nucleotides of the first and the second strand are located at opposing sites. In contrast to this the RNAi molecule comprised of strands 94A1 and 94B2 have the same pattern of modified and unmodified nucleotides. However, there is a phase shift such that the modified nucleotide forms base paring with an unmodified nucleotide. The two RNAi molecules comprised of strands 94A1 and 94B1 and strands 94A2 and 94B2 differ from each other such that in the first case the first strand starts with an unmodified nucleotide and the corresponding first nucleotide of the second strand, i. e. the nucleotide at the 3' end of the second strand, starts with an unmodified nucleotide with the arrangement being opposite to this in the RNAi molecule comprised of 94A2 and 94B2.

[0091] Additionally, alternatingly modified RNAi molecules as depicted in Fig. 12B are functional in mediating a PTEN protein knock down as shown in Fig. 12D but only when the second 5' and second 3' terminal nucleotide is not modified (see 94A294B1 and 94A294B2). Taken together these data show that the most stable and most active RNAi molecules do have alternating 2'Alkyl modified and unmodified nucleotide residues. It should be noted that these molecules do show a very similar mRNA reduction when compared to unmodified siRNA molecules which being stable in serum allows increased or easier handling.

Example 10: Functional Protein Knockdown mediated by internally modified RNAi molecules

[0092] The experimental approach was similar to the one outlined in connection with example 1.

[0093] Western Blots were performed on HeLa cells harvested at various time points following transfection (48, 72, 96 and 120 hours) with alternatingly modified RNAi molecules as depicted in Fig. 12B. For experimental reasons it is noteworthy that at the 96 hour time point cells have been split and half the population was replated. A total of 40 nM of the various RNAi molecules were applied to the cells. Cells were continuously transfected for 72h with cationic lipids as described in example 1; then replated in the absence of transfection reagents.

[0094] Transfections were carried out in 96 well or 10-cm plates (at 30% to 50% confluency) by using various cationic lipids such as Oligofectamine, Lipofectamine (Life Technologies), NC388, L8 (Atugen, Berlin), RNAi were transfected by adding pre-formed 5x concentrated complex of siRNAs and lipid in serum-free medium to cells in complete medium. The total transfection volume was 100 µl for cells plated in 96-wells and 10 ml for cells in 10 cm plates. The final lipid concentration was 0.8 to 1.2 µg/ml depending on cell density; the siRNA concentration is indicated in each experiment.

[0095] The result of the Western Blot analysis is depicted in Fig. 13. As can be taken from this Figure, modified RNAi molecules of the 94A2B1 and 94A2B2 version yield a longer lasting PTEN protein knock down as unmodified molecules. The lack of protein knock down also seen in Fig. 12 with molecules of the 94A1B1 and 94A1B2 version is confirmed in

this experiment. Unmodified molecules (80AB) are not as potent in supporting long lasting protein knock down when the cells are not continuously transfected.

Example 11: Persistent PTEN protein knock down with alternating 2'-O-methyl modifications of RNAi molecules

[0096] The experimental approach was similar to the one outlined in connection with example 10 with the exception that the transfection was terminated after 5 h by replacing the transfection medium with new medium. The protocol was slightly modified such that for each of the RNAi molecules a 40 nM concentration was realized using a stock solution of 1 µg RNAi / ml cationic lipid as described in connection with example 1. 5 hours after transfection the medium was withdrawn and fresh EMEM added. The cells were split after 72, with half of the cells being lysed and the other half newly plated and lysed 24 h later (96h post transfection). The result of a Western Blot analysis using 3 different RNAi molecules (80AB, 94A1/B2, 94A2/B1) are depicted in Fig. 14. As a positive control untreated cells were used. Fig. 14 shows the expression of PTEN after 72 h and 96 h, respectively. Taken the structural particularities of the various RNAi molecules it can be taken from Fig. 14 that protein knockdown is persistent with alternating molecules of the 94A2B1 kind even over 96 h after splitting and replating cells compared to unmodified RNAi molecules (such as 80AB) and RNAi molecule 94A1B2.

[0097] A further experiment was carried out using the siRNA constructs as depicted in Fig. 15A (left panel). From the results as depicted as ratio of PTEN/p110α mRNA degradation at the various concentrations of siRNA constructs administered to the test system, it can be taken that siRNA molecules with either one or both strands consisting of 2'-O-methyl residues were not able to induce RNA interference in the mammalian system (Fig. 15A, molecules V2, V5, V6). However, the decrease in activity was less pronounced when only parts of the strands were modified. Interestingly, a molecule having an unmodified antisense strand (which is the upper strand in the representation throughout this specification if not indicated otherwise) and a completely modified sense strand was significantly more active when compared to the reversed version (Fig. 5A, molecules V5 and V6). This result suggests that the antisense strand of the siRNA seems to be more critical and sensitive to modification. The most efficient molecules inducing PTEN mRNA had only stretches of modifications leaving the 5' end unmodified or were modified on alternating positions on both strands (Fig. 15A, molecules V10, V12).

[0098] To test the nuclease resistance the different siRNA versions were incubated in serum followed PAA gelectrophoresis. The result is shown in Fig. 15B (right panel with the various sequences indicated on the left panel of Fig. 15B). As shown earlier, blunt ended siRNA molecules with unmodified ribonucleotides were very rapidly degraded whereas a complete substitution with 2'-O-methyl nucleotides mediated resistance against serum-derived nucleases (Fig. 15B, compare molecule AB with V1). siRNA molecules with partial 2'-O-methyl modification showed as well an increased stability when compared to unmodified siRNAs. Especially molecules with alternating modifications on both strands showed a significant improve in instability (Fig. 15B, molecules V13, V14, V15 and V12). More importantly, transfection of three of these molecules into HeLa cells resulted in a significant down regulation of PTEN protein expression as depicted in Fig. 15C, length 6, 9 and 10). In this RNA interference activity assay an unexpected preference for molecules was observed which were modified at every second nucleotide beginning with the most 5' terminal nucleotide of the antisense strand (molecules V15 and V12). Molecules which contained modifications beginning with the second nucleotide at the 5' end of the antisense strand were more stable but had a strongly reduced activity in gene silencing (molecules V13, V14). This result points towards highly specific interactions between the involved enzymes and precise nucleotides in the siRNA duplex. Taken together the data shown herein demonstrate that 2'-O-methyl modifications at particularly selected positions in the siRNA duplex can increase nuclease resistance and do not necessarily abolish RNAi completely.

[0099] Although an increased stability of synthetic siRNA has primarily implication for *in vivo* application, it was also analysed whether the particular modification can also lead to an extended protein knock-down in cell culture systems. In accordance therewith HeLa cells were transiently transfected for six hours using different versions of PTEN specific siRNAs. The lipid siRNA complex was then washed away and the PTEN protein knock-down was analysed 48 hours and 120 hours later. Although knock-down experiments without continued transfection of siRNAs are complicated due to rapid growth of untransfected cells in this time period resulting in a very transient knock-down, the present inventors were able to demonstrate a prolonged PTEN protein knock-down with siRNA molecules stabilised by the described 2'-O-methyl modification. At 48 hours post transfection the unmodified siRNA (AB) showed the biggest reduction in PTEN protein levels, however, at 120 hours post transfection the reduction in PTEN protein expression is superior with the siRNA stabilised by alternating 2'-O-methyl modifications (Fig. 15D, compare lane 2 with lanes 4, 6 and 7).

[0100] From the results it can also be taken that preferably the starting nucleotide position of the alternating modification seems to be important. To test this preference in more detail two additional series of siRNAs were synthesised, one specific for the kinase Akt1 and the other one specific for p 110β which is one of the two catalytic subunits of PI(3-) kinase. The particular constructs are shown in Fig. 16A. As may be taken therefrom only 19 nt long siRNA duplexes either without any or with 2'-O-methyl modification on every second other nucleotide were used. Using Akt1 as a target

an efficient protein knock-down as well as a dramatic reduction in phospho-Akt levels was observed with blunt, unmodified siRNAs (Fig. 16A, right panel). From the different versions of molecules with modifications on every second other nucleotide only one was efficiently mediating RNAi (Fig. 16A, molecule V5). This siRNA molecule contained an antisense strand which was modified at the most terminal 5' and 3' nucleotides. The sense strand started with the unmodified 5 nucleotides at the most terminal position, resulting in a structure in which the modified and unmodified ribonucleotides of both strands are facing each other. As expected, this molecule was also protected against serum-derived nucleases as depicted in Fig. 16B (molecule V5).

[0101] Interestingly, a very similar 19 nt long siRNA molecule (V4) with modifications beginning at the second nucleotide of the antisense strand showed no RNA interference activation in the particular assay used. The version V6 in which the modified nucleotides of the antisense strand are facing modified nucleotides on the sense strand, was also inactive in this experiment. An identical series of 19 nt long siRNA molecules specific for p110 β confirmed these observations as depicted in Fig. 16C. Again the similarly modified siRNA molecule (V5) was the most active, as indicated by reducing Akt phosphorylation, which is indicative for a reduced P (I)-3 kinase activity due to reduced p110 β levels. The reduced activity of the molecules V6 might be explained by reduced duplex stability since the same structure was active in the 10 PTEN knock-down experiment with 21mer siRNAs. Although it is known that 2'-O-methyl modification on both strands facing each other will reduce the stability of nucleic acid duplexes, the difference between the activity of siRNA molecules 15 V4 and V5 (Figs. 16B and C) is probably not due to differences in duplex stability since the number of base pairing of modified and unmodified nucleotides is identical. This difference in activity might be due to specific requirements in the 20 interacting proteins involved in the degradation of the target mRNA. Also it can be taken from these experiments that the most terminal nucleotides of the antisense strand can be modified at the 2'-OH-group with significant loss of silencing activity.

Example 12: Different loop structures are functional in mediating RNA interference

[0102] To test whether RNAi molecules, preferably synthetic RNAi molecules with self complementary structures can inhibit gene expression as efficiently as standard double stranded siRNA molecules, HeLa cells were transfected with p110 β specific synthetic siRNAs. Transfections were carried out in 96 well or 10-cm plates (at 30% to 50% confluence) by using various cationic lipids such as Oligofectamine, Lipofectamine (Life Technologies), GeneBlocs were transfected by adding pre-formed 5x concentrated complex of GB and lipid in serum-free medium to cells in complete medium. The 30 total transfection volume was 100 μ l for cells plated in 96-wells and 10 ml for cells in 10 cm plates. The final lipid concentration was 0.8 to 1.2 μ g/ml depending on cell density; the RNAi molecule concentration is indicated in each experiment.

[0103] A dose dependent titration showed no significant difference in efficiency of mRNA knock-down achieved by the standard bimolecular double strand 21mer and the corresponding monomolecular molecules as analysed by realtime 35 PCR (Taqman) (Fig. 17A). Two different loop structures a (A)₁₂ loop and a HIV derived pA-loop were tested in parallel with similar results. A comparision of the relative position of the antisense sequence and the loop structure revealed an improved knock-down efficiency with the antisense sequence being located 3' to the loop (Fig. 17B; compare construct 3A, 3B and 4A, 4B).

Example 13: Studies on the efficacy of different intramolecular hairpin loops and intermolecular "bubbles"

[0104] The influence of different loop structures on inhibition of mRNA and protein expression was tested. For these experiments Akt1 and Akt2 were chosen as targets. The experimental approach was similar to the one described in example 12.

[0105] Significantly, the reduction in Akt1 mRNA as depicted in Fig. 18A and Fig. 18B as well as Akt1 protein levels as depicted in Fig. 18C was completely independent of the loop structure tested (compare molecules 5A, 6A, 7A, 8A) (the structure of the RNAi molecule tested is always depicted underneath the bar diagram). Even a molecule containing a rather unphysiological structure such as a polyethyleneglycol linker (PEG) as a loop efficiently reduced Akt1 expression indicating that size and nucleotide sequence of the loop is not crucial (Fig. 18A; molecule 8A). A synthetic siRNA molecule specific for Akt2 (9A) was used to control for specificity, and had no effect on Akt1 levels as shown in Fig. 15A. This molecule, however, efficiently silenced Akt2 expression (Fig. 18B; Fig. 18C). Self-complementary RNA molecules with loop structures have the possibility to anneal as doublestrands in monomolecular or bimolecular structures under physiological hybridization conditions (Fig. 18B, loop or bubble structure). To address the question of whether the siRNA molecules exert their function via adapting an intra-molecular loop or an inter-molecnlar "bubble" (schematically shown in Fig. 18B) two molecules not capable of folding back on themselves were transfected. These constructs contained Akt1- and Akt2-specific sequences within the same molecule (Fig. 18B, constructs 10A, 10B) and were designed to be restricted to form a bimolecular duplex ("bubble"). Surprisingly, this molecule efficiently mediated both Akt1 and Akt2 mRNA knock-down as well as protein knock-down when transfected after annealing of both strands.

[0106] Whether loop and bubble structures are indeed substrates for RNA processing enzymes, e.g. *Dicer*, is not clear at this point. A recent study by Paddison and coworkers suggests that hairpin containing siRNAs are more dependent on *Dicer* activity than double stranded siRNAs. However, these data demonstrating RNA interference activity using a PEG linker molecule indicate that the linker sequence is likely to be irrelevant.

5

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Claims

40 1. A ribonucleic acid comprising a double stranded structure, whereby the double stranded structure comprises a first
 strand and a second strand, whereby the first strand comprises a first stretch of contiguous nucleotides and whereby
 said first stretch is at least partially complementary to a target nucleic acid, and the second strand comprises a
 second stretch of contiguous nucleotides and whereby said second stretch is at least partially identical to the target
 nucleic acid,
 45 **characterised in**
 that said first stretch and said second stretch comprises a pattern consisting of a plurality of groups of modified
 nucleotides having a modification at the 2'-position whereby within the stretch each group of modified nucleotides
 is flanked on one or both sides by a flanking group of nucleotides whereby the flanking nucleotides forming the
 flanking group of nucleotides are either unmodified nucleotides or nucleotides having a modification different from
 50 the modification of the modified nucleotides.

2. The ribonucleic acid according to claim 1, wherein the group of modified nucleotides and/or the group of flanking
 nucleotides comprises a number of nucleotides whereby the number is selected from the group comprising one
 nucleotide to 10 nucleotides.

55 3. The ribonucleic acid according to any of claims 1 to 2, wherein the pattern of modified nucleotides of said first stretch
 is the same as the pattern of modified nucleotides of said second stretch.

4. The ribonucleic acid according to any of claims 1 to 3, wherein the pattern of said first stretch aligns with the pattern of said second stretch.
5. The ribonucleic acid according to claim 3, wherein the pattern of said first stretch is shifted by one or more nucleotides relative to the pattern of the second stretch.
6. The ribonucleic acid according to any of claims 1 to 5, wherein the modification is selected from the group comprising amino, fluoro, methoxy, alkoxy and alkyl.
10. 7. The ribonucleic acid according to any of claims 1 to 6, wherein the double stranded structure is blunt ended.
8. The ribonucleic acid according to any of claims 1 to 7, wherein the double stranded structure is blunt ended on both sides.
15. 9. The ribonucleic acid according to any of claims 1 to 7, wherein the double stranded structure is blunt ended on the side on the double stranded structure which is defined by the 5'-end of the first strand and the 3'-end of the second strand.
20. 10. The nucleic acid according to any of claims 1 to 7, wherein the double stranded structure is blunt ended on the side on the double stranded structure which is defined by the 3'-end of the first strand and the 5'-end of the second strand.
11. The ribonucleic acid according to any of claims 1 to 6, wherein the first strand comprises an overhang at the 5'-end and the second strand comprises an overhang at the 5'-end.
25. 12. The ribonucleic acid according to any of claims 1 to 6, wherein both strands have an overhang of at least one nucleotide at the 3'-end.
13. The ribonucleic acid according to claim 11 or 12, wherein the overhang consists of at least one nucleotide which is selected from the group comprising ribonucleotides and deoxyribonucleotides.
30. 14. The ribonucleic acid according to claim 13, wherein the nucleotide has a modification, whereby said modification is preferably selected from the group comprising nucleotides being an inverted abasic and nucleotides having an NH₂-modification at the 2'-position.
35. 15. The ribonucleic acid according to any of claims 1 to 14, wherein the length of the double-stranded structure has a length from about 17 to 21 and more preferably 18 or 19 bases.
16. The ribonucleic acid according to any of claims 1 to 7 and 9 to 14, wherein the length of said first strand and the length of said second strand is independently from each other selected from the group comprising the ranges of from about 15 to about 23 bases, 17 to 21 bases and 18 or 19 bases.
40. 17. The ribonucleic acid according to claim 15, wherein the length of said first strand and the length of said second strand is independently from each other selected from the group comprising the ranges from 17 to 21 bases and 18 or 19 bases.
45. 18. The ribonucleic acid according to any of claims 1 to 17, wherein the complementarity between said first strand and the target nucleic acid is perfect.
19. The ribonucleic acid according to any of claims 1 to 17, wherein the duplex formed between the first strand and the target nucleic acid comprises at least 15 nucleotides wherein there is one mismatch or two mismatches between said first strand and the target nucleic acid forming said double-stranded structure.
50. 20. The ribonucleic acid according to any of claims 1 to 3 and 5 to 19 to the extent they are not referring to claim 4, wherein both the first strand and the second strand each comprise a pattern consisting of a plurality of groups of modified nucleotides and a plurality of flanking group of nucleotides, whereby each group of modified nucleotides comprises at least one nucleotide and whereby each flanking group of nucleotides comprising at least one nucleotide; with each group of modified nucleotides of the first strand being aligned with a flanking group of nucleotides on the

second strand, whereby

the most terminal 5' nucleotide of the first strand is a nucleotide of the group of modified nucleotides, and the most terminal 3' nucleotide of the second strand is a nucleotide of the flanking group of nucleotides.

5 **21.** The ribonucleic acid according to claim 20, wherein each group of modified nucleotides consists of a single nucleotide and/or each flanking group of nucleotides consists of a single nucleotide.

10 **22.** The ribonucleic acid according to claim 21, wherein on the first strand the nucleotide forming the flanking group of nucleotides is an unmodified nucleotide which is arranged in a 3' direction relative to the nucleotide forming the group of modified nucleotides, and wherein on the second strand the nucleotide forming the group of modified nucleotides is a modified nucleotide which is arranged in 5' direction relative to the nucleotide forming the flanking group of nucleotides.

15 **23.** The ribonucleic acid according to any of claims 20 to 22, wherein the first strand comprises eight to twelve, preferably nine to eleven, groups of modified nucleotides, and wherein the second strand comprises seven to eleven, preferably eight to ten, groups of modified nucleotides.

20 **24.** The ribonucleic acid according to any of claims 1 to 6, whereby the first strand and the second strand are linked by a loop structure.

25 **25.** The ribonucleic acid according to claim 24, wherein the loop structure is comprised of a non-nucleic acid polymer.

30 **26.** The ribonucleic acid according to claim 25, **characterised in that** the non-nucleic acid polymer is polyethylene glycol.

35 **27.** The ribonucleic acid according to claim 24, wherein the loop structure is comprised of a nucleic acid.

40 **28.** The ribonucleic acid according to any of claims 24 to 27, **characterised in that** the 5'-terminus of the first strand is linked to the 3'-terminus of the second strand.

45 **29.** The ribonucleic acid according to any of claims 24 to 27, **characterised in that** the 3'-end of the first strand is linked to the 5'-terminus of the second strand.

50 **30.** The ribonucleic acid according to any of claims 1 to 29, wherein the target gene is selected from the group comprising structural genes, housekeeping genes, transcription factors, motility factors, cell cycle factors, cell cycle inhibitors, enzymes, growth factors, cytokines and tumor suppressors.

55 **31.** Use of a ribonucleic acid according to any of claims 1 to 30, for target validation.

60 **32.** Use of a ribonucleic acid according to any of claims 1 to 30 for the manufacture of a medicament.

65 **33.** The use according to claim 32, wherein the medicament is for the treatment of a disease or of a condition which is selected from the group comprising glioblastoma, prostate cancer, breast cancer, lung cancer, liver cancer, colon cancer, pancreatic cancer and leukaemia, diabetes, obesity, cardiovascular diseases, and metabolic diseases.

70 **34.** A cell, preferably a knockdown cell, containing a ribonucleic acid according to any of claims 1 to 30, whereby if the cell is a human cell, the human cell is an isolated human cell.

75 **35.** An organism, preferably a knockdown organism, containing a ribonucleic acid according to any of claims 1 to 30, whereby the organism is different from a human being.

80 **36.** A composition containing a ribonucleic acid according to any of claims 1 to 30.

85 **37.** A pharmaceutical composition containing a ribonucleic acid according to any of claims 1 to 30 and a pharmaceutically acceptable carrier.

90 **38.** An in vitro method for inhibiting the expression of a target gene in a cell or derivative thereof comprising introducing a ribonucleic acid according to any of claims 1 to 30 into the cell in an amount sufficient to inhibit expression of the target gene, wherein the target gene is the target gene of the ribonucleic acid according to any of claims 1 to 30.

Patentansprüche

1. Ribonukleinsäure umfassend eine doppelsträngige Struktur, wobei die doppelsträngige Struktur einen ersten Strang und einen zweiten Strang umfasst, wobei der erste Strang einen ersten Abschnitt aus aufeinanderfolgenden Nukleotiden umfasst und wobei der erste Abschnitt wenigstens teilweise komplementär zu einer Ziel-Nukleinsäure ist, und der zweite Strang einen zweiten Abschnitt aus aufeinanderfolgenden Nukleotiden umfasst, wobei der zweite Strang wenigstens teilweise identisch ist zu der Ziel-Nukleinsäure,
dadurch gekennzeichnet, dass
 der erste Abschnitt und der zweite Abschnitt ein Muster umfassen bestehend aus einer Vielzahl von Gruppen aus modifizierten Nukleotiden mit einer Modifikation einer 2'-Position, wobei innerhalb des Abschnittes jede Gruppe aus modifizierten Nukleotiden auf einer oder beiden Seiten von einer flankierenden Gruppe von Nukleotiden flankiert ist, wobei die flankierenden Nukleotide, die die flankierende Gruppe von Nukleotiden ausbilden, entweder unmodifizierte Nukleotide oder Nukleotide sind mit einer Modifikation, die von der Modifikation der modifizierten Nukleotide verschieden ist.
2. Ribonukleinsäure nach Anspruch 1, wobei die Gruppe aus modifizierten Nukleotiden und/oder die Gruppe aus flankierenden Nukleotiden eine Anzahl von Nukleotiden umfasst, wobei die Anzahl ausgewählt ist aus der Gruppe bestehend aus einem Nukleotid bis 10 Nukleotide.
3. Ribonukleinsäure nach einem der Ansprüche 1 bis 2, wobei das Muster aus modifizierten Nukleotiden des ersten Abschnittes das gleiche ist wie das Muster aus modifizierten Nukleotiden des zweiten Abschnittes.
4. Ribonukleinsäure nach einem der Ansprüche 1 bis 3, wobei das Muster des ersten Abschnittes mit dem Muster des zweiten Abschnittes ausgerichtet ist.
5. Ribonukleinsäure nach Anspruch 3, wobei das Muster des ersten Abschnittes um ein oder mehrere Nukleotide relativ zum Muster des zweiten Abschnittes verschoben ist.
6. Ribonukleinsäure nach Anspruch 1 bis 5, wobei die Modifikation ausgewählt ist aus der Gruppe umfassend Amino, Fluoro, Methoxy, Alkoxy und Alkyl.
7. Ribonukleinsäure nach einem der Ansprüche 1 bis 6, wobei die doppelsträngige Struktur glattendig ist.
8. Ribonukleinsäure nach einem der Ansprüche 1 bis 7, wobei die doppelsträngige Struktur auf beiden Seiten glattendig ist.
9. Ribonukleinsäure nach einem der Ansprüche 1 bis 7, wobei die doppelsträngige Struktur auf der Seite der doppelsträngigen Struktur glattendig ist, die durch das 5'-Ende des ersten Stranges und das 3'-Ende des zweiten Stranges definiert ist.
10. Ribonukleinsäure nach einem der Ansprüche 1 bis 7, wobei die doppelsträngige Struktur auf der Seite der doppelsträngigen Struktur glattendig ist, die durch das 3'-Ende des ersten Stranges und das 5'-Ende des zweiten Stranges definiert ist.
11. Ribonukleinsäure nach einem der Ansprüche 1 bis 6, wobei der erste Strang einen Überhang am 5'-Ende umfasst und der zweite Strang einen Überhang am 5'-Ende umfasst.
12. Ribonukleinsäure nach einem der Ansprüche 1 bis 6, wobei beide Stränge einen Überhang aus wenigstens einem Nukleotid am 3'-Ende aufweisen.
13. Ribonukleinsäure nach Anspruch 11 oder 12, wobei der Überhang aus wenigstens einem Nukleotid besteht, das ausgewählt ist aus der Gruppe umfassend Ribonukleotide und Desoxyribonukleotide.
14. Ribonukleinsäure nach Anspruch 13, wobei das Nukleotid eine Modifikation aufweist, wobei die Modifikation bevorzugterweise ausgewählt ist aus der Gruppe umfassend Nukleotide, die ein invertiertes abasisches Nukleotid sind, und Nukleotide mit einer NH₂-Modifikation am 2'-Ende.
15. Ribonukleinsäure nach einem der Ansprüche 1 bis 14, wobei die Länge der doppelsträngigen Struktur eine Länge

von etwa 17 bis 21 und bevorzugterweise 18 oder 19 Basen aufweist.

- 5 16. Ribonukleinsäure nach einem der Ansprüche 1 bis 7 und 9 bis 14, wobei die Länge des ersten Stranges und die Länge des zweiten Stranges unabhängig voneinander ausgewählt sind aus der Gruppe umfassend die Bereiche von etwa 15 bis etwa 23 Basen, 17 bis 21 Basen und 18 oder 19 Basen.
- 10 17. Ribonukleinsäure nach Anspruch 15, wobei die Länge des ersten Stranges und die Länge des zweiten Stranges unabhängig voneinander ausgewählt sind aus der Gruppe umfassend die Bereiche von 17 bis 21 Basen und 18 oder 19 Basen.
- 15 18. Ribonukleinsäure nach einem der Ansprüche 1 bis 17, wobei die Komplementarität zwischen dem ersten Strang und der Ziel-Nukleinsäure vollständig ist.
- 20 19. Ribonukleinsäure nach einem der Ansprüche 1 bis 17, wobei der zwischen dem ersten Strang und der Ziel-Nukleinsäure ausgebildete Duplex wenigstens 15 Nukleotide umfasst, wobei ein oder zwei Fehlpaarungen zwischen dem ersten Strang und der Ziel-Nukleinsäure vorhanden ist/sind, die die doppelsträngige Struktur ausbilden.
- 25 20. Ribonukleinsäure nach einem der Ansprüche 1 bis 3 und 5 bis 19, in dem Umfang, wie sie sich nicht auf Anspruch 4 beziehen, wobei sowohl der erste Strang als auch der zweite Strang jeweils ein Muster umfassen bestehend aus einer Vielzahl von Gruppen aus modifizierten Nukleotiden und einer Vielzahl von flankierenden Gruppen von Nukleotiden, wobei jede Gruppe aus modifizierten Nukleotiden wenigstens ein Nukleotid umfasst und wobei eine jede flankierende Gruppe von Nukleotiden wenigstens ein Nukleotid umfasst, wobei eine jede Gruppe aus modifizierten Nukleotiden des ersten Stranges mit einer flankierenden Gruppe von Nukleotiden an dem zweiten Strang ausgerichtet ist, wobei das am meisten terminal gelegene 5'-Nukleotid des ersten Stranges ein Nukleotid der Gruppe aus modifizierten Nukleotiden ist, und das am meisten terminal gelegene 3'-Nukleotid des zweiten Stranges ein Nukleotid der flankierenden Gruppe von Nukleotiden ist.
- 30 21. Ribonukleinsäure nach Anspruch 20, wobei jede Gruppe aus modifizierten Nukleotiden aus einem einzelnen Nukleotid besteht und/oder jede flankierende Gruppe von Nukleotiden aus einem einzelnen Nukleotid besteht.
- 35 22. Ribonukleinsäure nach Anspruch 21, wobei auf dem ersten Strang das Nukleotid, das die flankierende Gruppe von Nukleotiden ausbildet, ein unmodifiziertes Nukleotid ist, das in 3'-Richtung relativ zu dem Nukleotid angeordnet ist, das die Gruppe aus modifizierten Nukleotiden ausbildet, und wobei auf dem zweiten Strang das Nukleotid, das die Gruppe aus modifizierten Nukleotiden ausbildet, ein modifiziertes Nukleotid ist, das in 5'-Richtung relativ zu dem Nukleotid angeordnet ist, das die flankierende Gruppe von Nukleotiden bildet.
- 40 23. Ribonukleinsäure nach einem der Ansprüche 20 bis 22, wobei der erste Strang acht bis zwölf, bevorzugterweise neun bis elf Gruppen aus modifizierten Nukleotiden umfasst und wobei der zweite Strang sieben bis elf, bevorzugterweise acht bis zehn Gruppen aus modifizierten Nukleotiden umfasst.
- 45 24. Ribonukleinsäure nach einem der Ansprüche 1 bis 6, wobei der erste Strang und der zweite Strang durch eine Schleifen-Struktur verbunden sind.
25. Ribonukleinsäure nach Anspruch 24, wobei die Schleifen-Struktur ein Nicht-Nukleinsäure-Polymer umfasst.
- 50 26. Ribonukleinsäure nach Anspruch 25, **dadurch gekennzeichnet, dass** das Nicht-Nukleinsäure-Polymer Polyethylenglycol ist.
27. Ribonukleinsäure nach Anspruch 24, wobei die Schleifen-Struktur eine Nukleinsäure umfasst.
- 55 28. Ribonukleinsäure nach einem der Ansprüche 24 bis 27, **dadurch gekennzeichnet, dass** der 5'-Terminus des ersten Stranges mit dem 3'-Terminus des zweiten Stranges verknüpft ist.
29. Ribonukleinsäure nach einem der Ansprüche 24 bis 27, **dadurch gekennzeichnet, dass** das 3'-Ende des ersten Stranges mit dem 5'-Terminus des zweiten Stranges verknüpft ist.

30. Ribonukleinsäure nach einem der Ansprüche 1 bis 29, wobei das Zielgen ausgewählt ist aus der Gruppe umfassend Strukturgene, Hauskeeping-Gene, Transkriptionsfaktoren, Motilitätsfaktoren, Zellzyklusfaktoren, Zellzyklusinhibitoren, Enzyme, Wachstumsfaktoren, Zytokine und Tumorsuppressoren.

5 31. Verwendung einer Ribonukleinsäure nach einem der Ansprüche 1 bis 30 zur Target-Validierung.

32. Verwendung einer Ribonukleinsäure nach einem der Ansprüche 1 bis 30 für die Herstellung eines Medikaments.

10 33. Verwendung nach Anspruch 32, wobei das Medikament für die Behandlung einer Erkrankung oder eines Zustandes ist, die/der ausgewählt ist aus der Gruppe umfassend Glioblastome, Prostatakrebs, Brustkrebs, Lungenkrebs, Leberkrebs, Kolonkrebs, Pankreaskrebs und Leukämie, Diabetes, Fettleiblichkeit, kardiovaskuläre Erkrankungen und metabolische Erkrankungen.

15 34. Zelle, bevorzugterweise eine Knockdown-Zelle, enthaltend eine Ribonukleinsäure nach einem der Ansprüche 1 bis 30, wobei wenn die Zelle eine menschliche Zelle ist, die menschliche Zelle eine isolierte menschliche Zelle ist.

35. Organismus, bevorzugterweise Knockdown-Organismus, der eine Ribonukleinsäure nach einem der Ansprüche 1 bis 30 enthält, wobei der Organismus verschieden ist von einem Menschen.

20 36. Zusammensetzung umfassend eine Ribonukleinsäure nach einem der Ansprüche 1 bis 30.

37. Pharmazeutische Zusammensetzung umfassend eine Ribonukleinsäure nach einem der Ansprüche 1 bis 30 und einen pharmazeutisch akzeptablen Träger.

25 38. In vitro Verfahren zur Inhibierung der Expression eines Zielgens in einer Zelle oder einem Derivat davon, umfassend das Einführen einer Ribonukleinsäure nach einem der Ansprüche 1 bis 30 in die Zelle in einer Menge, die ausreicht, um die Expression des Zielgens zu inhibieren, wobei das Zielgen das Zielgen der Ribonukleinsäure nach einem der Ansprüche 1 bis 30 ist.

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Revendications

1. Acide ribonucléique comprenant une structure double brin, dans lequel la structure double brin comprend un premier brin et un second brin, dans laquelle le premier brin comprend une première élongation de nucléotides contigus et dans laquelle ladite première élongation est au moins partiellement complémentaire d'un acide nucléique cible, et le second brin comprend une seconde élongation de nucléotides contigus et dans laquelle ladite seconde élongation est au moins partiellement identique à l'acide nucléique cible,
caractérisé en ce que

35 ladite première élongation et ladite seconde élongation comprennent un motif consistant en une pluralité de groupes de nucléotides modifiés ayant une modification à la position 2' dans laquelle, à l'intérieur de l'élongation, chaque groupe de nucléotides modifiés est flanqué sur un ou deux de ses côtés par un groupe de nucléotides flanquants dans lequel les nucléotides flanquants formant le groupe de nucléotides flanquants sont soit des nucléotides non modifiés, soit des nucléotides ayant une modification différente de la modification des nucléotides modifiés.

40 2. Acide ribonucléique selon la revendication 1, dans lequel le groupe de nucléotides modifiés et/ou le groupe de nucléotides flanquants comprend un nombre de nucléotides dans lequel le nombre est sélectionné dans le groupe comprenant de un nucléotide à 10 nucléotides.

45 3. Acide ribonucléique selon l'une quelconque des revendications 1 à 2, dans lequel le motif de nucléotides modifiés de ladite première élongation est le même que le motif de nucléotides modifiés de ladite seconde élongation.

50 4. Acide ribonucléique selon l'une quelconque des revendications 1 à 3, dans lequel le motif de ladite première élongation s'aligne avec le motif de ladite seconde élongation.

55 5. Acide ribonucléique selon la revendication 3, dans lequel le motif de ladite première élongation est remplacé par un ou plusieurs nucléotides par rapport au motif de la seconde élongation.

6. Acide ribonucléique selon l'une quelconque des revendications 1 à 5, dans lequel la modification est sélectionnée

dans le groupe comprenant amino, fluoro, méthoxyle, alkoxyde et alkyle.

7. Acide ribonucléique selon l'une quelconque des revendications 1 à 6, dans lequel la structure double brin comporte une extrémité franche.

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8. Acide ribonucléique selon l'une quelconque des revendications 1 à 7, dans lequel la structure double brin comporte une extrémité franche sur ses deux côtés.

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9. Acide ribonucléique selon l'une quelconque des revendications 1 à 7, dans lequel la structure double brin comporte une extrémité franche sur le côté de la structure double brin qui est définie par l'extrémité 5' du premier brin et l'extrémité 3' du second brin.

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10. Acide nucléique selon l'une quelconque des revendications 1 à 7, dans lequel la structure double brin comporte une extrémité franche sur le côté de la structure double brin qui est définie par l'extrémité 3' du premier brin et l'extrémité 5' du second brin.

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11. Acide ribonucléique selon l'une quelconque des revendications 1 à 6, dans lequel le premier brin comprend un décalage à l'extrémité 5' et le second brin comprend un décalage à l'extrémité 5'.

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12. Acide ribonucléique selon l'une quelconque des revendications 1 à 6, dans lequel les deux brins comportent un décalage d'au moins un nucléotide à l'extrémité 3'.

13. Acide ribonucléique selon la revendication 11 ou 12, dans lequel le décalage consiste en au moins un nucléotide qui est sélectionné dans le groupe comprenant des ribonucléotides et des désoxyribonucléotides.

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14. Acide ribonucléique selon la revendication 13, dans lequel le nucléotide possède une modification, dans laquelle ladite modification est de préférence sélectionnée dans le groupe comprenant des nucléotides qui sont un site abasique inversé et des nucléotides ayant une modification NH₂ à la position 2'.

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15. Acide nucléique selon l'une quelconque des revendications 1 à 14, dans lequel la longueur de la structure double brin est longue d'environ 17 à 21, et de manière plus préférée, 18 à 19 bases.

16. Acide ribonucléique selon l'une quelconque des revendications 1 à 7 et 9 à 14, dans lequel la longueur dudit premier brin et la longueur dudit second brin sont sélectionnées indépendamment l'une de l'autre dans le groupe comprenant les plages d'environ 15 à environ 23 bases, de 17 à 21 bases et de 18 à 19 bases.

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17. Acide ribonucléique selon la revendication 15, dans lequel la longueur dudit premier brin et la longueur dudit second brin sont sélectionnées indépendamment l'une de l'autre dans le groupe comprenant les plages de 17 à 21 bases et de 18 ou 19 bases.

18. Acide ribonucléique selon l'une quelconque des revendications 1 à 17, dans lequel la complémentarité entre ledit premier brin et l'acide nucléique cible est parfaite.

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19. Acide ribonucléique selon l'une quelconque des revendications 1 à 17, dans lequel le duplex formé entre le premier brin et l'acide nucléique cible comprend au moins 15 nucléotides dans lesquels il existe un mésappariement ou deux mésappariements entre ledit premier brin et l'acide nucléique cible formant ladite structure double brin.

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20. Acide ribonucléique selon l'une quelconque des revendications 1 à 3 et 5 à 19 dans la mesure où elle ne font pas référence à la revendication 4, dans laquelle à la fois le premier brin et le second brin comprennent chacun un motif consistant en une pluralité de groupes de nucléotides modifiés et en une pluralité de groupes de nucléotides flanquants, dans lesquels chaque groupe de nucléotides modifiés comprend au moins un nucléotide et dans lesquels chaque groupe de nucléotides flanquants comprend au moins un nucléotide ; avec chaque groupe de nucléotides modifiés du premier brin est aligné avec un groupe de nucléotides flanquants sur le second brin, dans lequel le nucléotide le plus 5' terminal du premier brin est un nucléotide du groupe de nucléotides modifiés, et le nucléotide le plus 3' terminal du second brin est un nucléotide du groupe de nucléotides flanquants.

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21. Acide ribonucléique selon la revendication 20, dans lequel chaque groupe de nucléotides modifiés consiste en un seul nucléotide et/ou chaque groupe de nucléotides flanquants consiste en un seul nucléotide.

5 22. Acide ribonucléique selon la revendication 21, dans lequel, sur le premier brin, le nucléotide formant le groupe de nucléotides flanquants est un nucléotide non modifié qui est disposé dans un sens 3' par rapport au nucléotide formant le groupe de nucléotides modifiés, et dans lequel, sur le second brin, le nucléotide formant le groupe de nucléotides modifiés est un nucléotide modifié qui est disposé dans un sens 5' par rapport au nucléotide formant le groupe de nucléotides flanquants.

10 23. Acide ribonucléique selon l'une quelconque des revendications 20 à 22, dans lequel le premier brin comprend huit à douze, de préférence neuf à onze, groupes de nucléotides modifiés, et dans lequel le second brin comprend sept à onze, de préférence huit à dix, groupes de nucléotides modifiés.

15 24. Acide ribonucléique selon l'une quelconque des revendications 1 à 6, dans lequel le premier brin et le second brin sont liés par une structure en boucle.

25. Acide ribonucléique selon la revendication 24, dans lequel la structure en boucle est composée d'un polymère n'étant pas constitué par un acide nucléique.

20 26. Acide ribonucléique selon la revendication 25, **caractérisé en ce que** le polymère n'étant pas constitué par un acide nucléique est un polyéthylène glycol.

27. Acide ribonucléique selon la revendication 24, dans lequel la structure en boucle est constituée d'un acide nucléique.

25 28. Acide ribonucléique selon l'une quelconque des revendications 24 à 27, **caractérisé en ce que** l'extrémité 5'-terminale du premier brin est liée à l'extrémité 3'-terminale du second brin.

29. Acide ribonucléique selon l'une quelconque des revendications 24 à 27, **caractérisé en ce que** l'extrémité 3' du premier brin est liée à l'extrémité 5'-terminale du second brin.

30 30. Acide ribonucléique selon l'une quelconque des revendications 1 à 29, dans lequel le gène cible est sélectionné dans le groupe comprenant des gènes structuraux, des gènes domestiques, des facteurs de transcription, des facteurs de motilité, des facteurs de cycle cellulaire, des inhibiteurs de cycle cellulaire, des enzymes, des facteurs de croissance, des cytokines et des suppresseurs de tumeurs.

35 31. Utilisation d'un acide ribonucléique selon l'une quelconque des revendications 1 à 30, pour une validation de cible.

32. Utilisation d'un acide nucléique selon l'une quelconque des revendications 1 à 30 pour la fabrication d'un médicament.

40 33. Utilisation selon la revendication 32, dans laquelle le médicament est destiné au traitement d'une maladie ou d'une affection qui est sélectionnée dans le groupe comprenant glioblastome, cancer de la prostate, cancer du sein, cancer du poumon, cancer du foie, cancer du côlon, cancer du pancréas et leucémie, diabète, obésité, maladies cardio-vasculaires, et maladies métaboliques.

45 34. Cellule, de préférence une cellule knock-down, contenant un acide ribonucléique selon l'une quelconque des revendications 1 à 30, dans laquelle si la cellule est une cellule humaine, la cellule humaine est une cellule humaine isolée.

50 35. Organisme, de préférence un organisme knock-down, contenant un acide ribonucléique selon l'une quelconque des revendications 1 à 30, dans lequel l'organisme est différent d'un être humain.

36. Composition contenant un acide ribonucléique selon l'une quelconque des revendications 1 à 30.

55 37. Composition pharmaceutique contenant un acide ribonucléique selon l'une quelconque des revendications 1 à 30 et un transporteur pharmaceutiquement acceptable.

38. Procédé *in vitro* pour inhiber l'expression d'un gène cible dans une cellule ou un dérivé de celle-ci comprenant l'introduction d'un acide ribonucléique, selon l'une quelconque des revendications 1 à 30, dans la cellule en une

quantité suffisante pour inhiber l'expression du gène cible, dans lequel le gène cible est le gène cible de l'acide ribonucléique selon l'une quelconque des revendications 1 à 30.

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Fig. 1

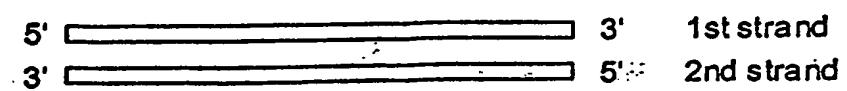


Fig. 2

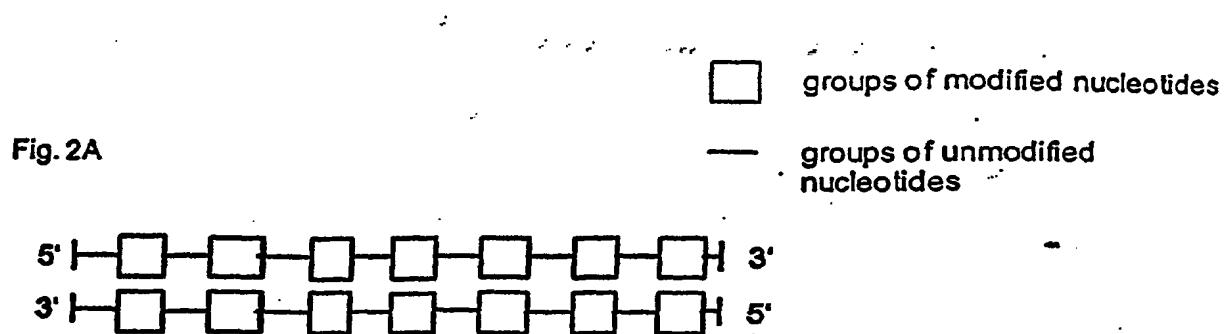


Fig. 2B

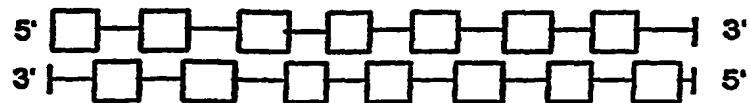


Fig. 2C

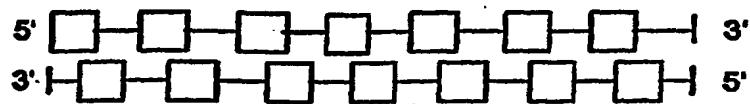
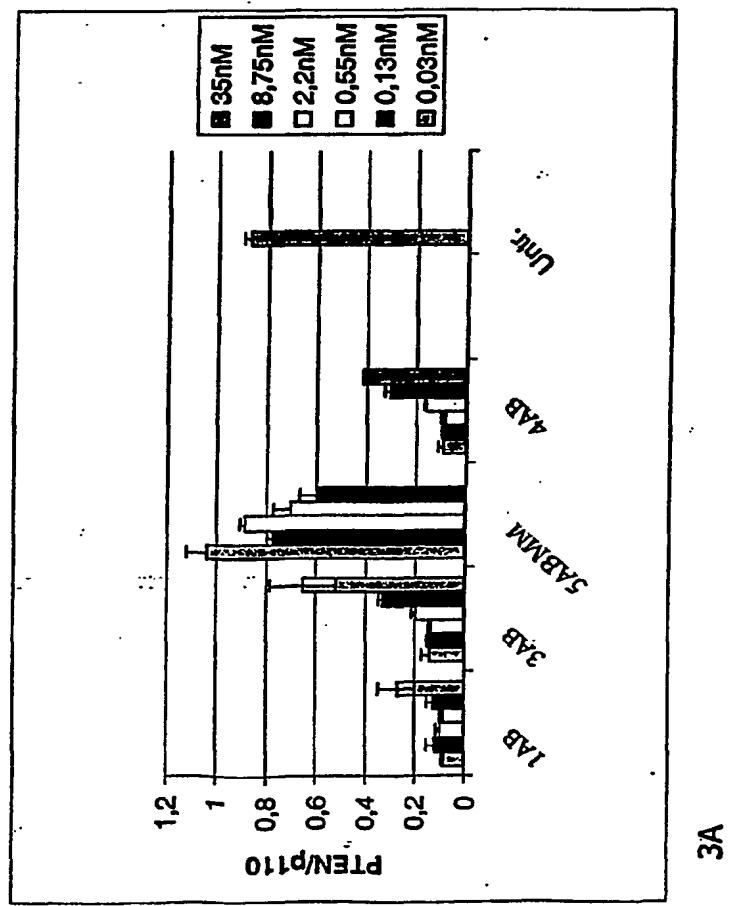


Fig.3



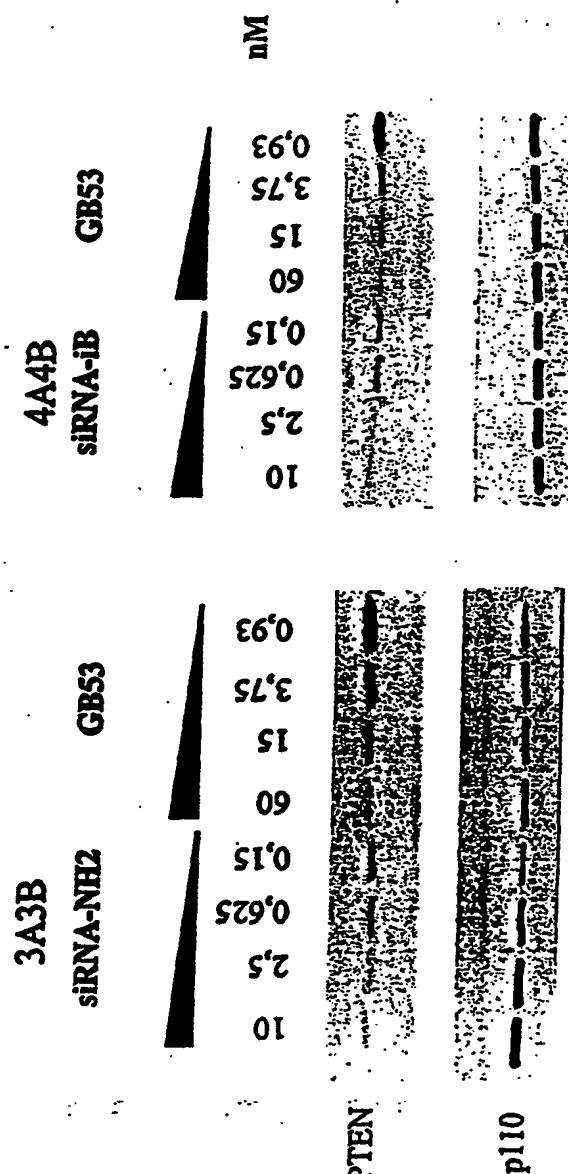
ONLY RNA WITH 2 DEOXY AT EACH END
 1A 5' - cuccuuuuguuucugcuacg-**TT**
 1B 3' -TT-gaggaaaaacaaacgcauugc

ONLY RNA WITH NH2 GROUPS AT EACH 3' END AND 2 DEOXY
 3A 5' - cuccuuuuguuucugcuacg-**TT-NH2**
 3B 3' -NH2-**TT**-gaggaaaaacaaacgcauugc

ONLY RNA WITH INVERTED ABASIC AND 2 TT
 4. 16153-1B (1B at the 3' ends)
 4A 5' - cuccuuuuguuucugcuacg-**TT-1B**
 4B 3' -**1B-TT**-gaggaaaaacaaacgcauugc

ONLY RNA WITH 2 DEOXY AT EACH END
 5A/B 5' - cuccuuuuguuucugcuacg-**TT**
 5B/B 3' -TT-gaggaaaaacaaacgcauugc

3B



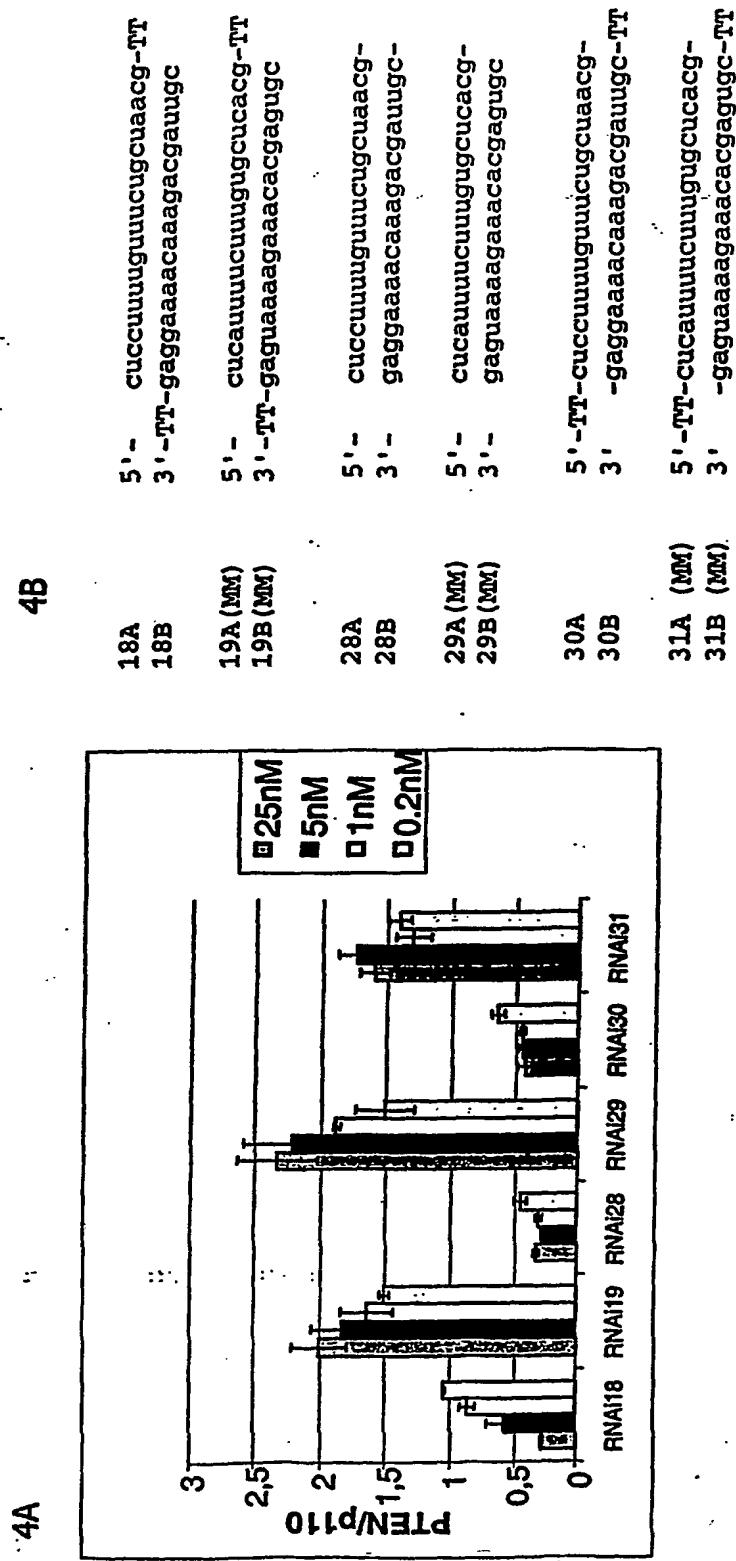


Fig. 4

Fig. 5

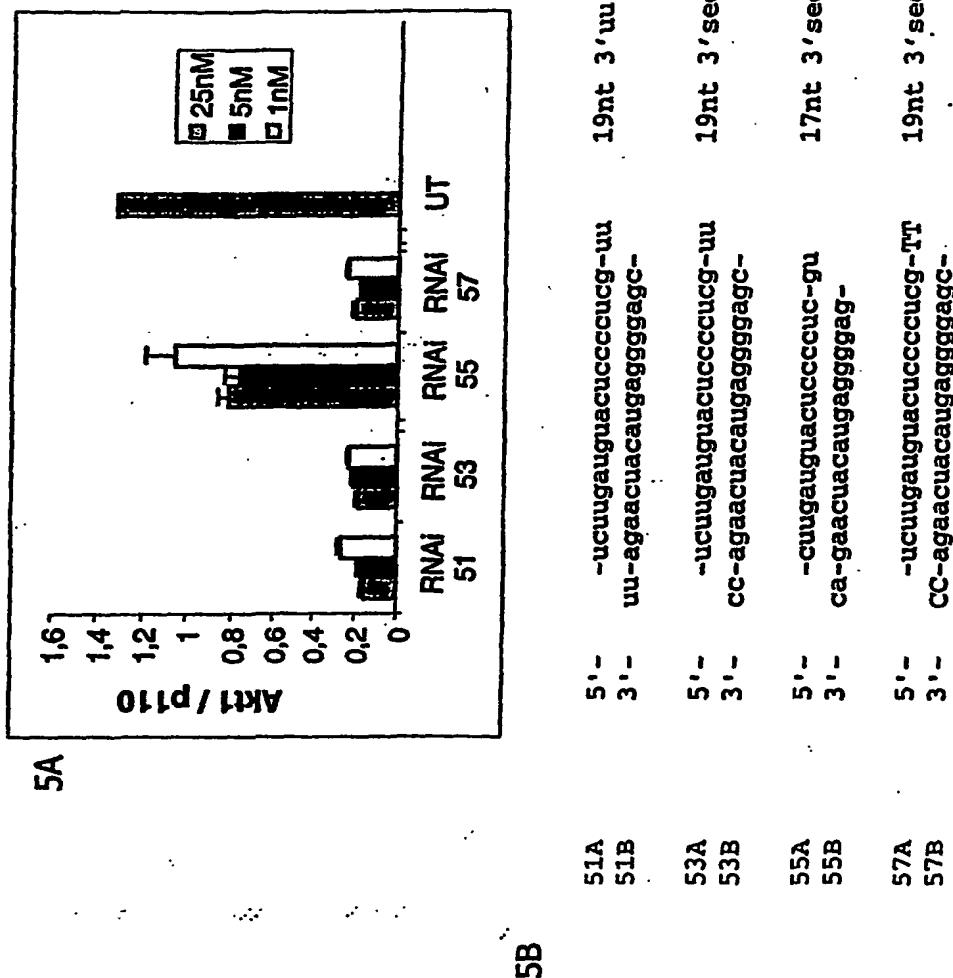
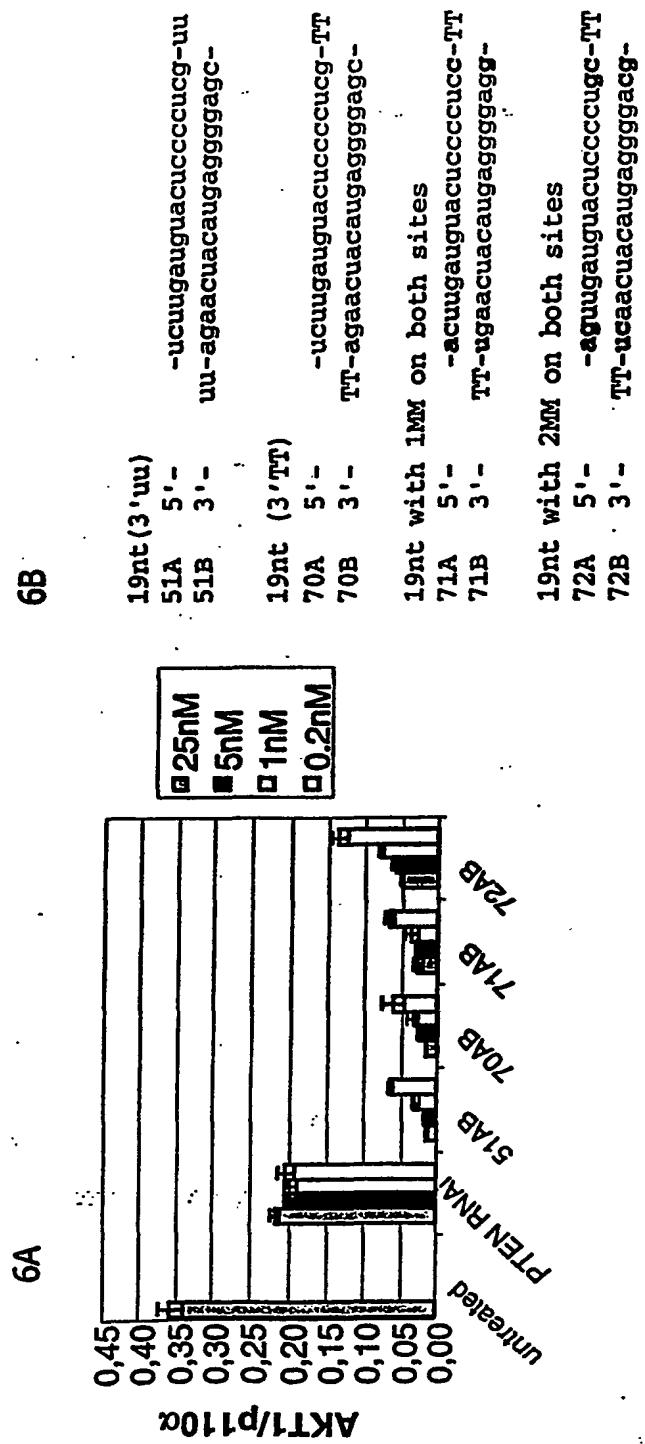


Fig. 6



A

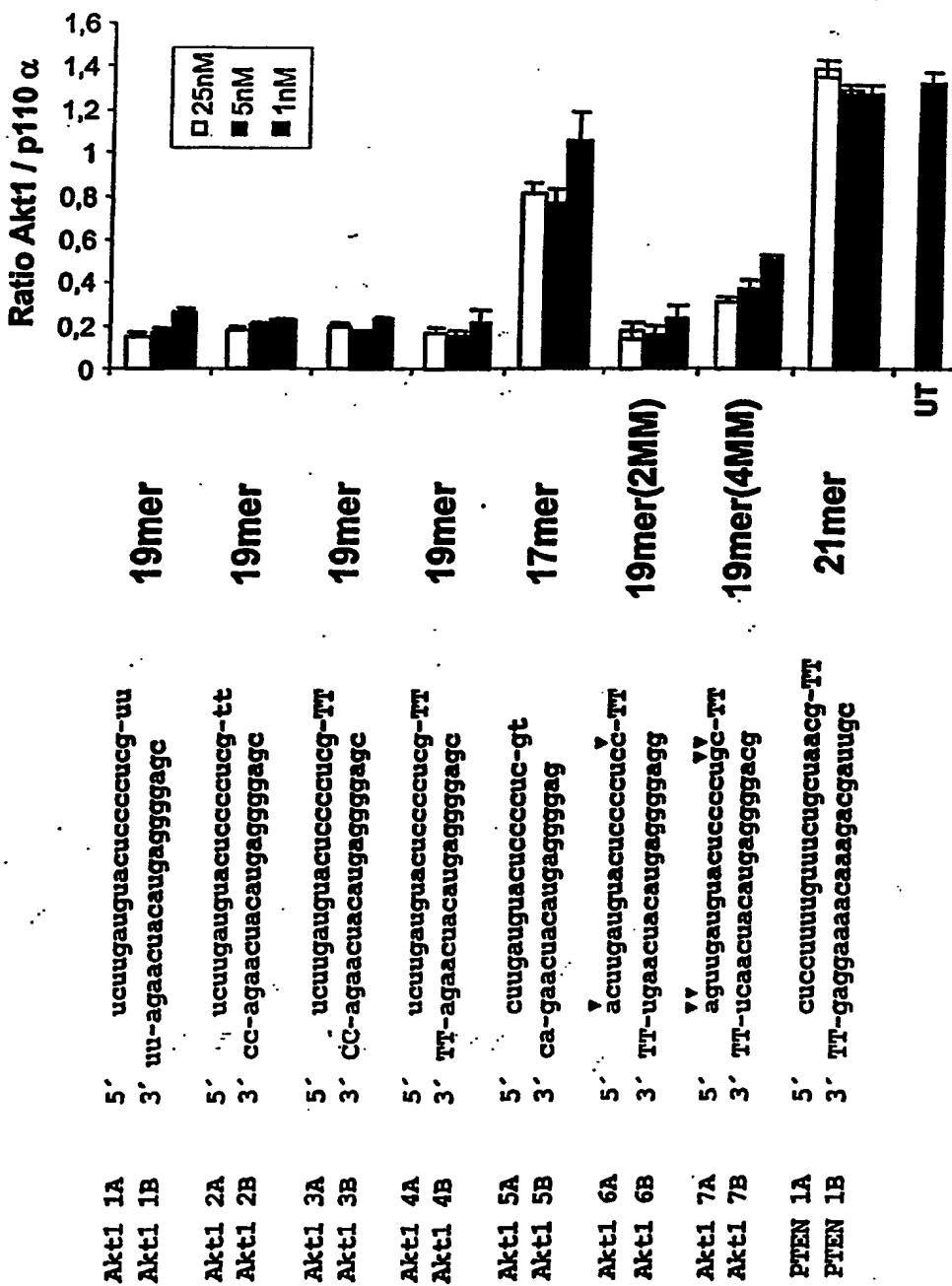


Fig. 7

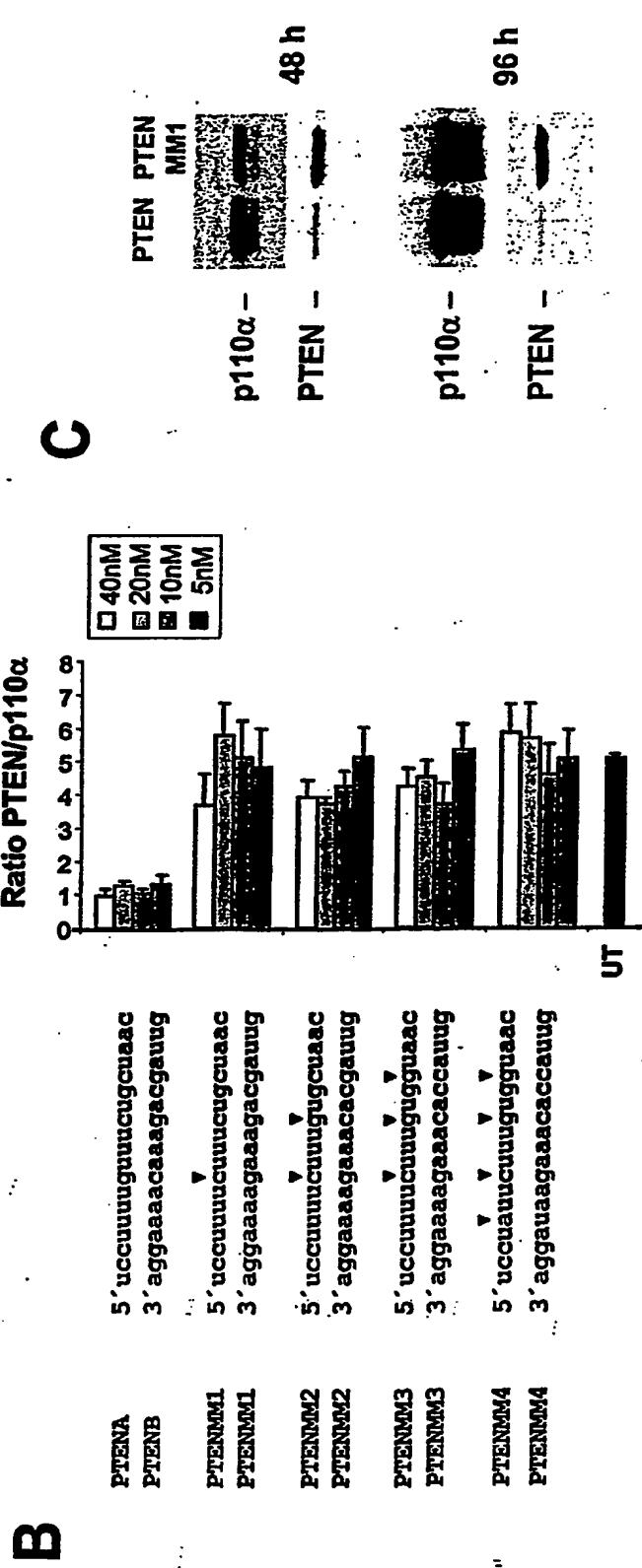
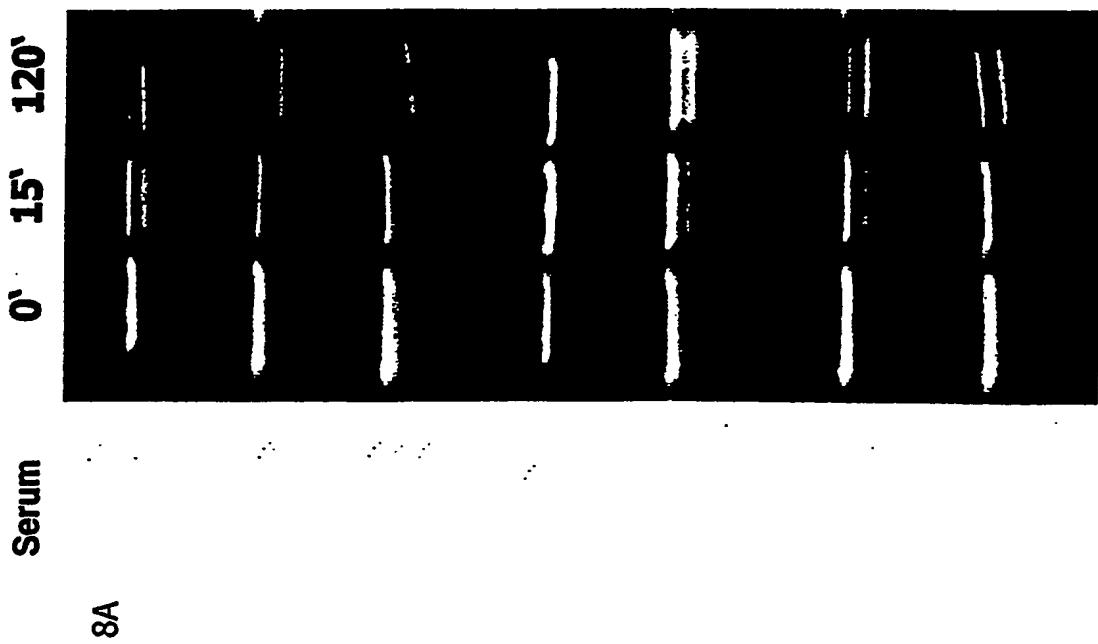


Fig. 7

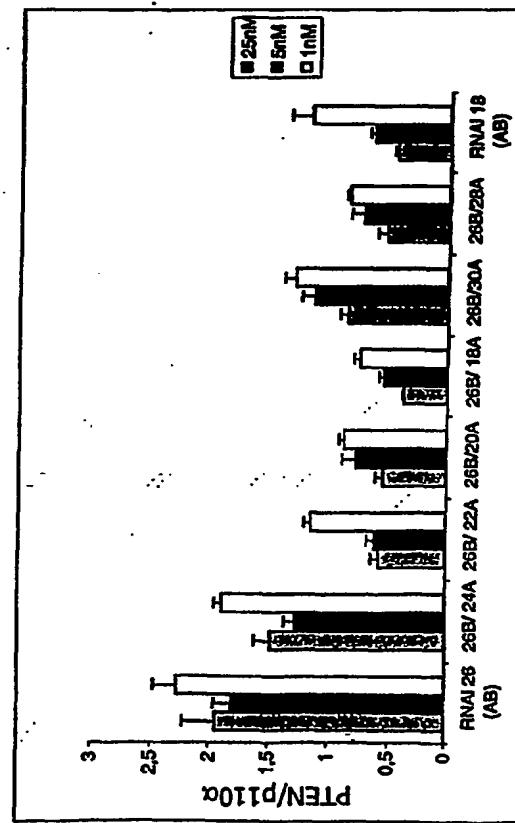
Fig. 8'



	Tuschi1	8B
18A	5' - cuccuuuuguuuucugcuuaacg- <u>TT</u> 3' - <u>iB</u> -cuccuuuuguuuucugcuuaacg- <u>TT</u> -iB	
18B	3' -TT-gaggaaaaacaaaggacgauugc	
	inverted abasic on both ends and 2' <u>TT</u>	
24A	5' - <u>iB</u> -cuccuuuuguuuucugcuuaacg- <u>TT</u> -iB	
24B	3' - <u>iB</u> - <u>TT</u> -gaggaaaaacaaaggacgauugc-iB	
	NH ₂ groups at both ends AND 2'-deoxy	
26A	5' - NH ₂ -cuccuuuuguuuucugcuuaacg- <u>TT</u> -NH ₂	
26B	3' -NH ₂ - <u>TT</u> -gaggaaaaacaaaggacgauugc-NH ₂	
	21-O-Methyl1 modified with 2'-deoxy at each end	
79A	5' - cuccuuuuguuuucugcuuaacg- <u>TT</u>	
79B	3' - <u>TT</u> -gaggaaaaacaaaggacgauugc	
	Only RNA	
28A	5' - cuccuuuuguuuucugcuuaacg- 3' - gaggaaaaacaaaggacgauugc	
28B	, 3' -	
	Only RNA with 2'-deoxy at each 5' end	
30A	5' - cuccuuuuguuuucugcuuaacg- 3' - <u>TT</u> -cuccuuuuguuuucugcuuaacg- <u>TT</u> -NH ₂	
30B	3' - <u>TT</u> -gaggaaaaacaaaggacgauugc- <u>TT</u>	
	NH ₂ groups at each 3' end and 2'-deoxy	
3A	5' - cuccuuuuguuuucugcuuaacg- <u>TT</u> -NH ₂	
3B	3' -NH ₂ - <u>TT</u> -gaggaaaaacaaaggacgauugc-	

Fig. 9

9A 9B



5' - NH2-cuccuuuuguuucugcuuacg-TT-NH2
3' - NH2-TT-gaggaaaacaagacgauugc-NH2

5' - iB-cuccuuuuguuucugcuuacg-TT-iB
3' - NH2-TT-gaggaaaacaagacgauugc-NH2

5' - cuccuuuuguuucugcuuacg-TT-NH2
3' - NH2-TT-gaggaaaacaagacgauugc-NH2

5' - TT-cuccuuuuguuucugcuuacg-
3' - NH2-TT-gaggaaaacaagacgauugc-NH2

5' - cuccuuuuguuucugcuuacg-
3' - NH2-TT-gaggaaaacaagacgauugc-NH2

5' - cuccuuuuguuucugcuuacg-TT
3' - TT-gaggaaaacaagacgauugc

9C

functional

functional

functional

not functional

functional

functional

functional

Fig. 10

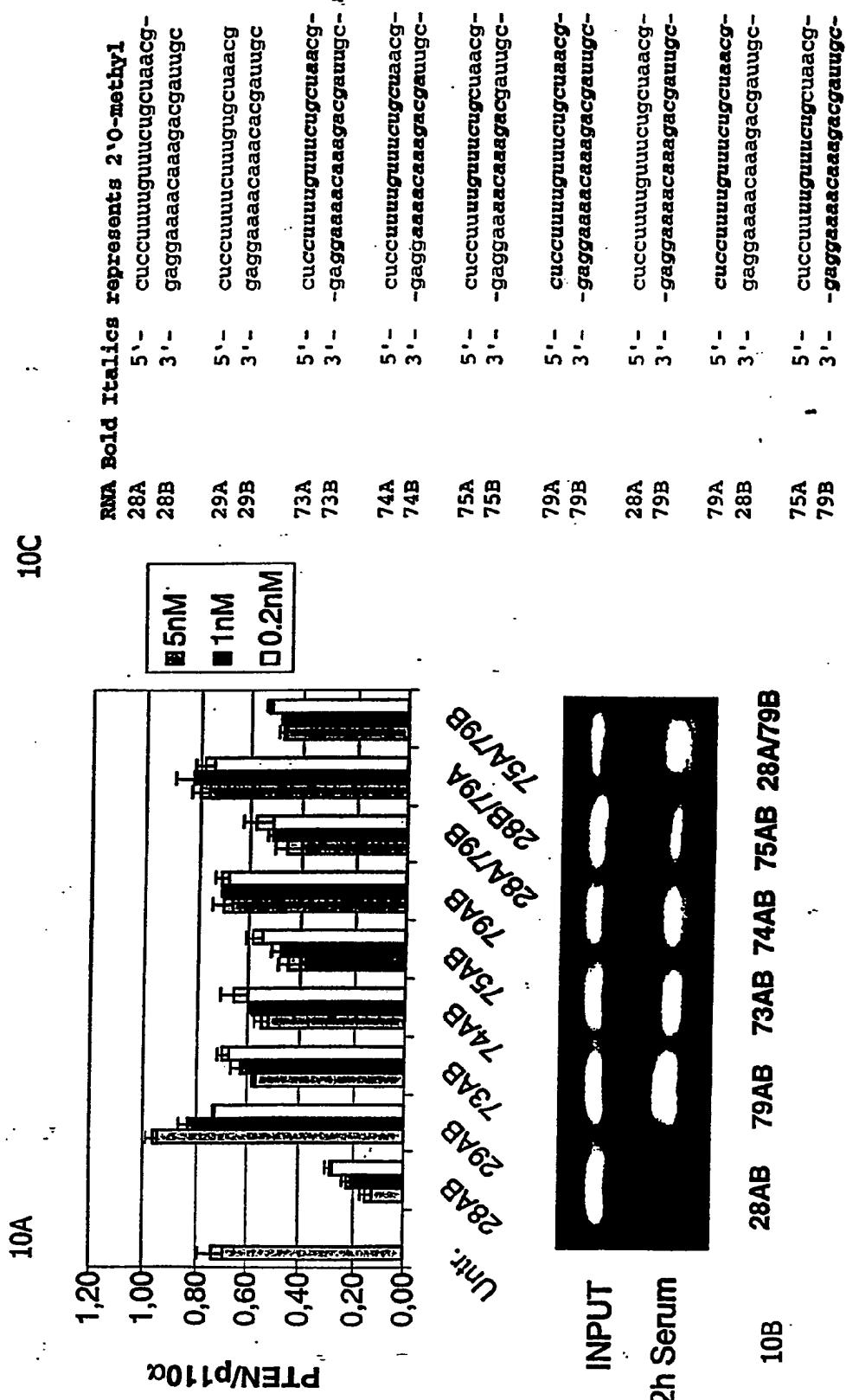
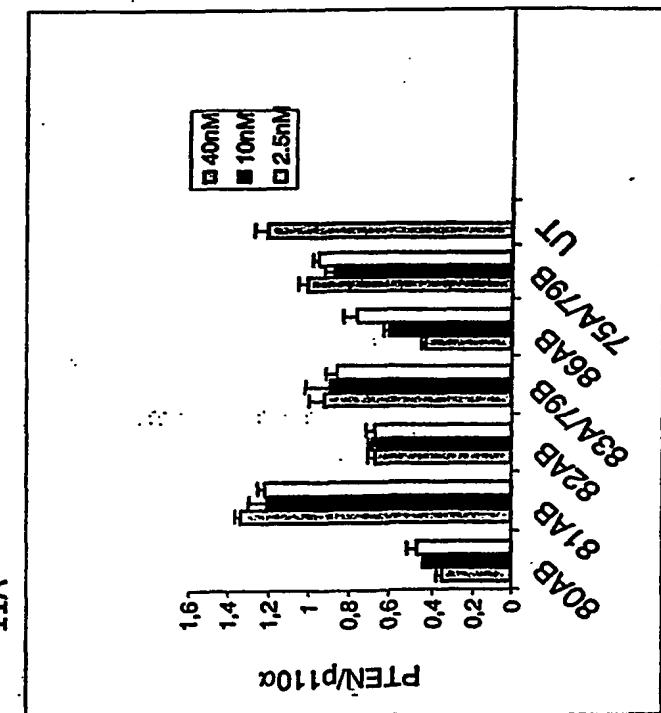


Fig. 1



11C

RNA *Bold Italics* represents 2'-O-methyl

-cucuuuuuuuuuuuuuuuuu-
-gaggaaaaacaaaaacggaaaaac-

CULTURE AND CIVILISATION

-gaggaaaaacaaggacggacggc-

ggggaaaaacaaaaacgauugc-
cuccuuuuuuguuuuuuuuuuuuuu-

cuccuuuuguuuucguuacg-
-ggggaaaaacaaaaacccggcc-

cuccuuuuuuucgguuacg-

-ggggaaaaacaaaaacgggg-

11B INPUT

2h Serum

80AB **82AB** **86AB** **75A** **79B**

Fig. 12

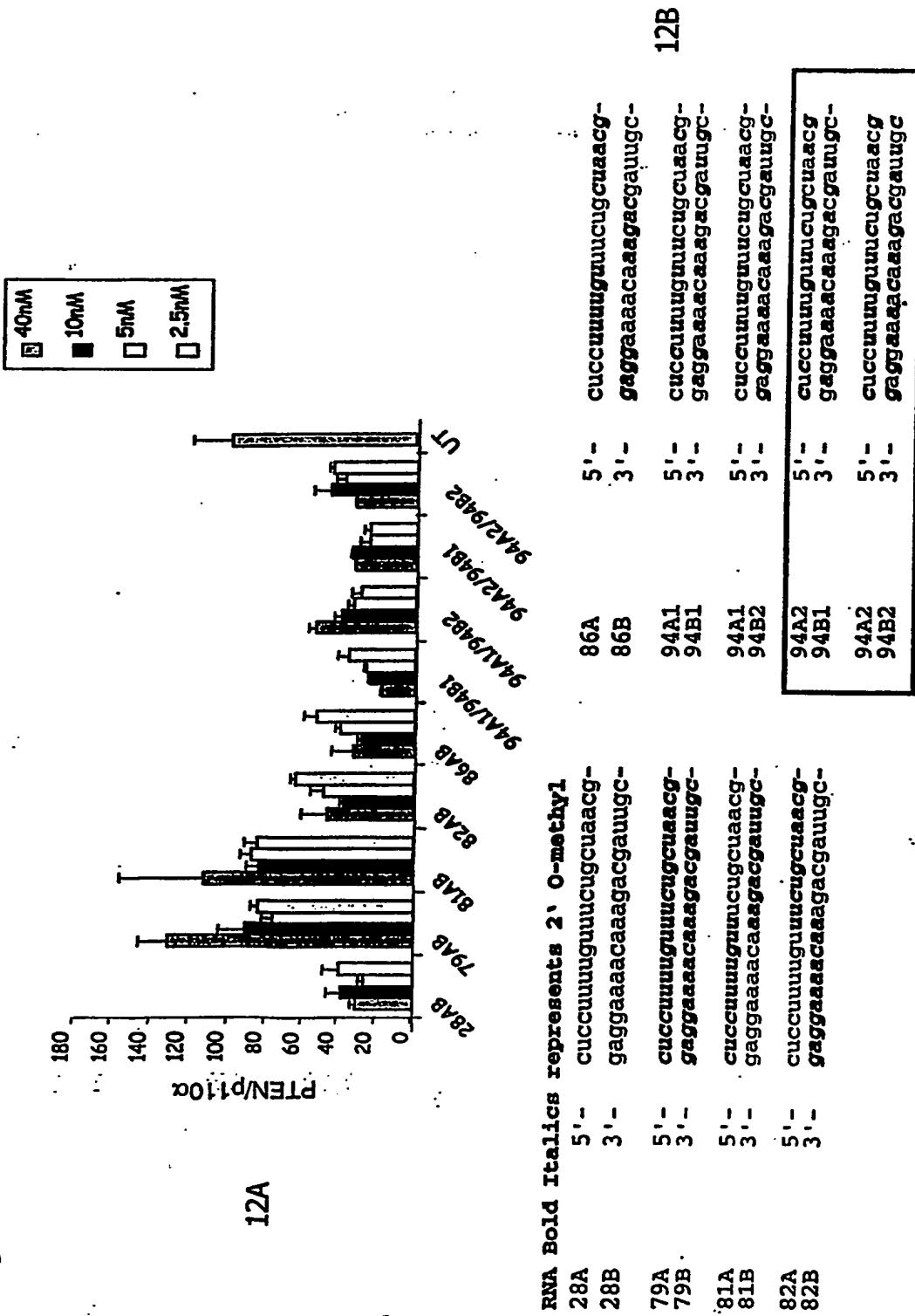
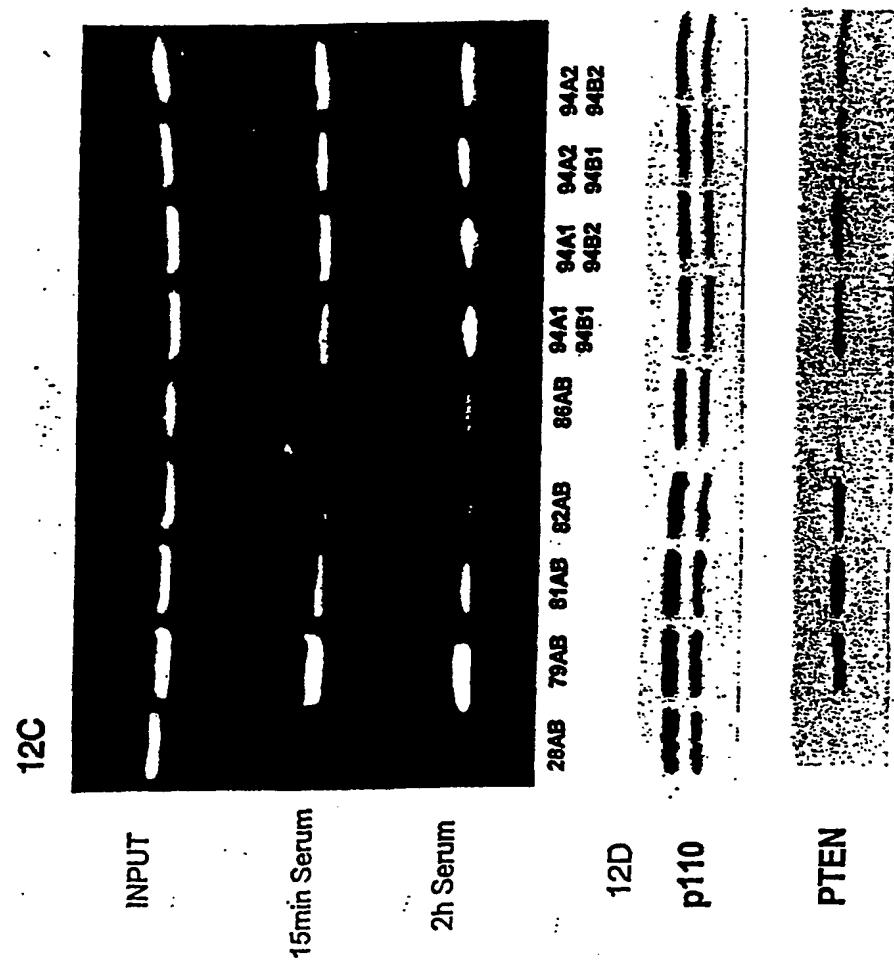
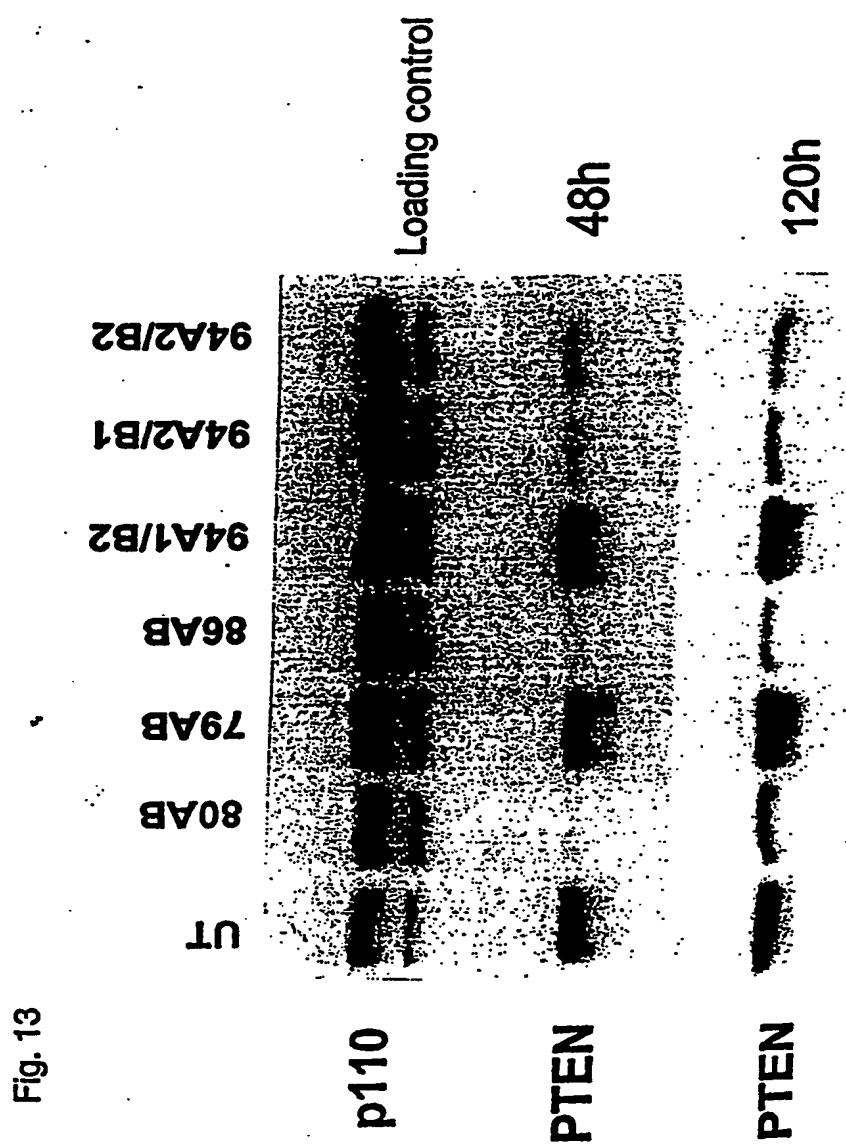


Fig. 12





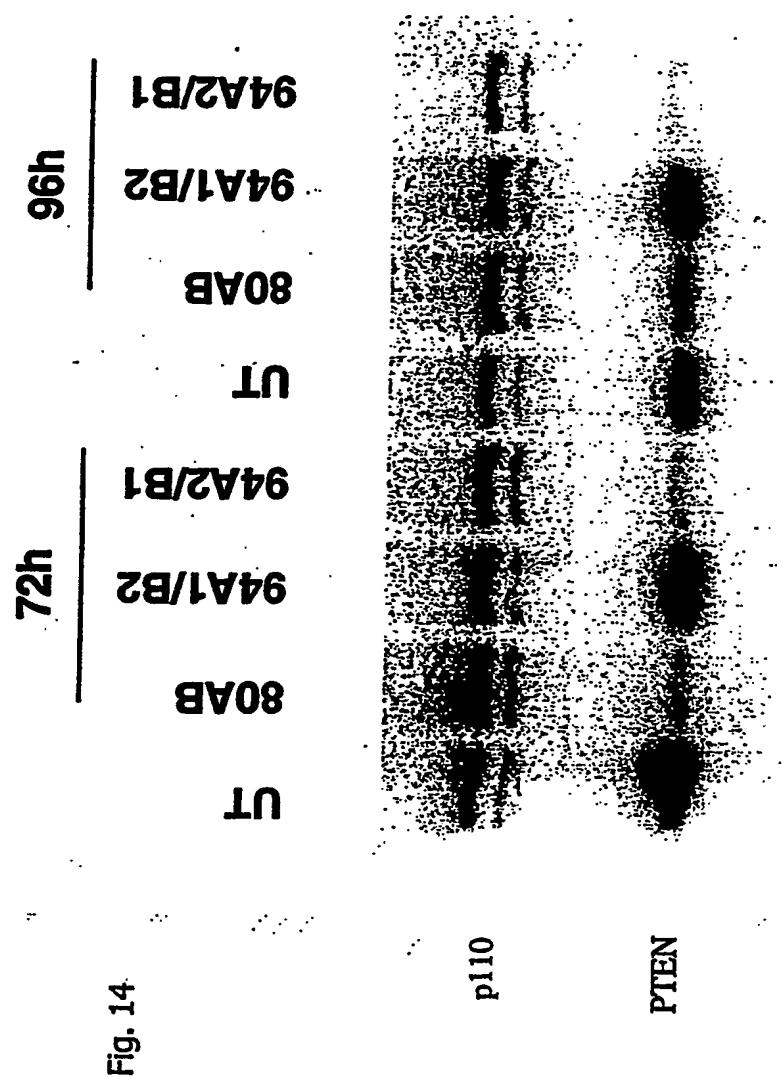


Fig. 14.

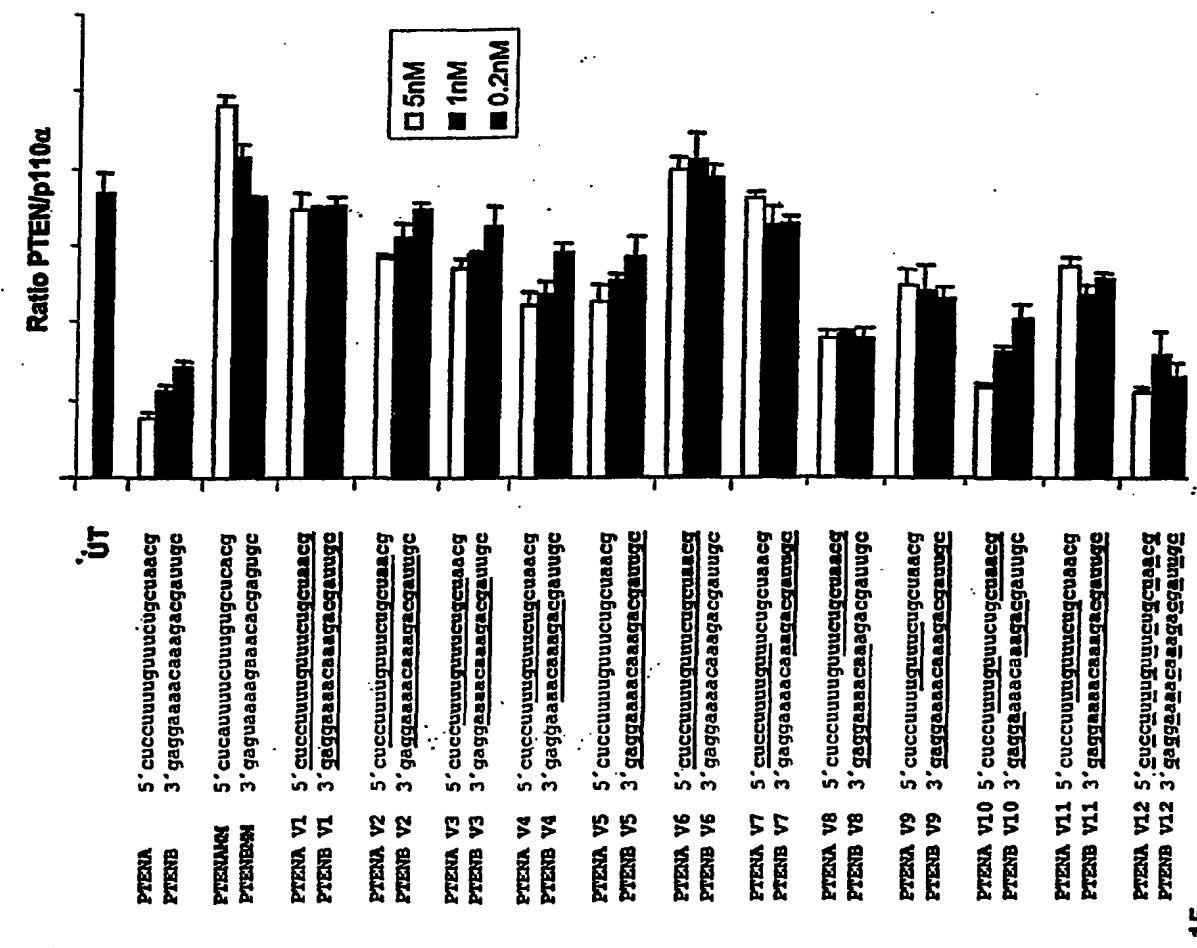


Fig. 15

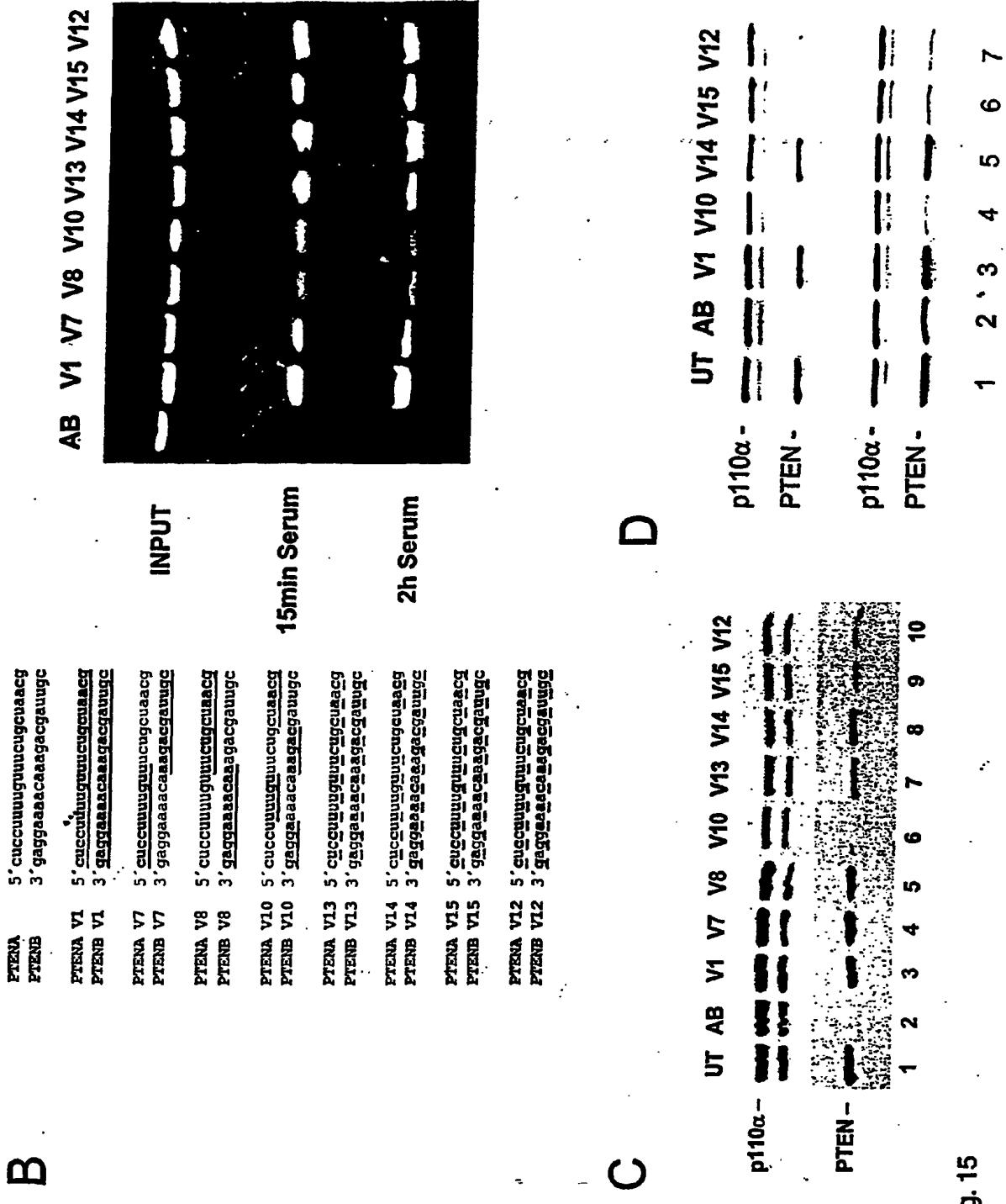
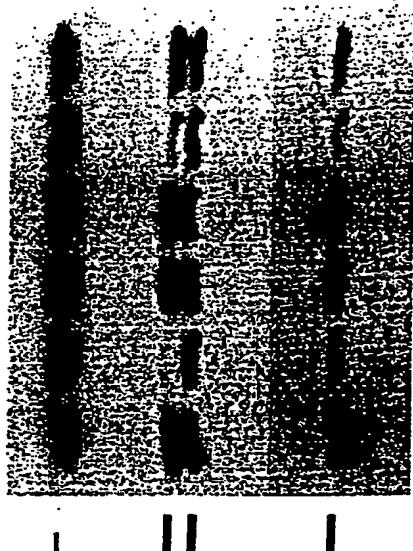


Fig. 15

A

		UT	V2	V3	V4	V5	V6
Akt1A	V1	5' ucuu <u>guau</u> ac <u>ucc</u> cc <u>ucg</u> -TT					
Akt1B	V1	3' TT- <u>agaac</u> u <u>cau</u> gggg <u>gg</u> gc					
Akt1A	V2	5' uc <u>u</u> gu <u>guau</u> ac <u>ucc</u> cc <u>ucg</u>					
Akt1B	V2	3' <u>agaac</u> u <u>cau</u> gggg <u>gg</u> gc					
Akt1A	V3	5' uc <u>u</u> gu <u>guau</u> ac <u>ucc</u> cc <u>ucg</u>					
Akt1B	V3	3' <u>agaac</u> u <u>cau</u> gggg <u>gg</u> gc					
Akt1A	V4	5' uc <u>u</u> gu <u>guau</u> ac <u>ucc</u> cc <u>ucg</u>					
Akt1B	V4	3' <u>agaac</u> u <u>cau</u> gggg <u>gg</u> gc					
Akt1A	V5	5' uc <u>u</u> gu <u>guau</u> ac <u>ucc</u> cc <u>ucg</u>					
Akt1B	V5	3' <u>agaac</u> u <u>cau</u> gggg <u>gg</u> gc					
Akt1A	V6	5' uc <u>u</u> gu <u>guau</u> ac <u>ucc</u> cc <u>ucg</u>					
Akt1B	V6	3' <u>agaac</u> u <u>cau</u> gggg <u>gg</u> gc					



B



INPUT

2h Serum

Fig. 16

C

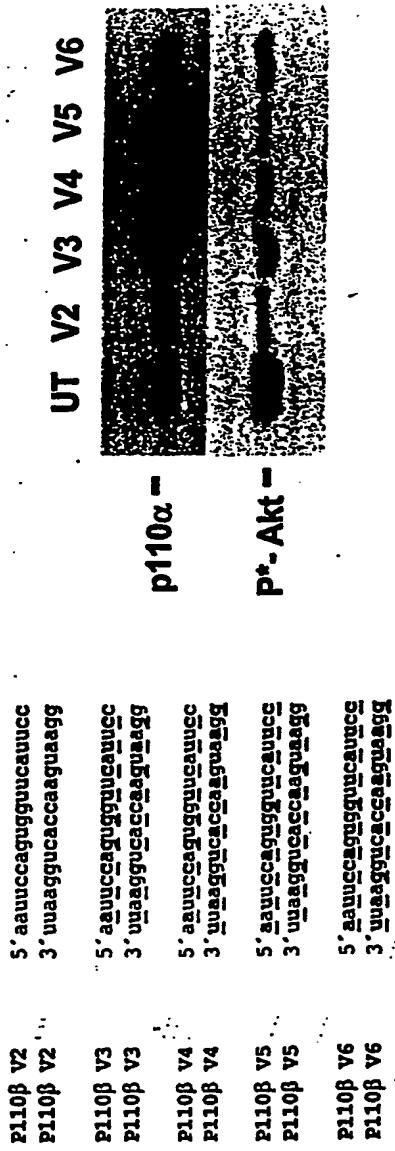


Fig. 16

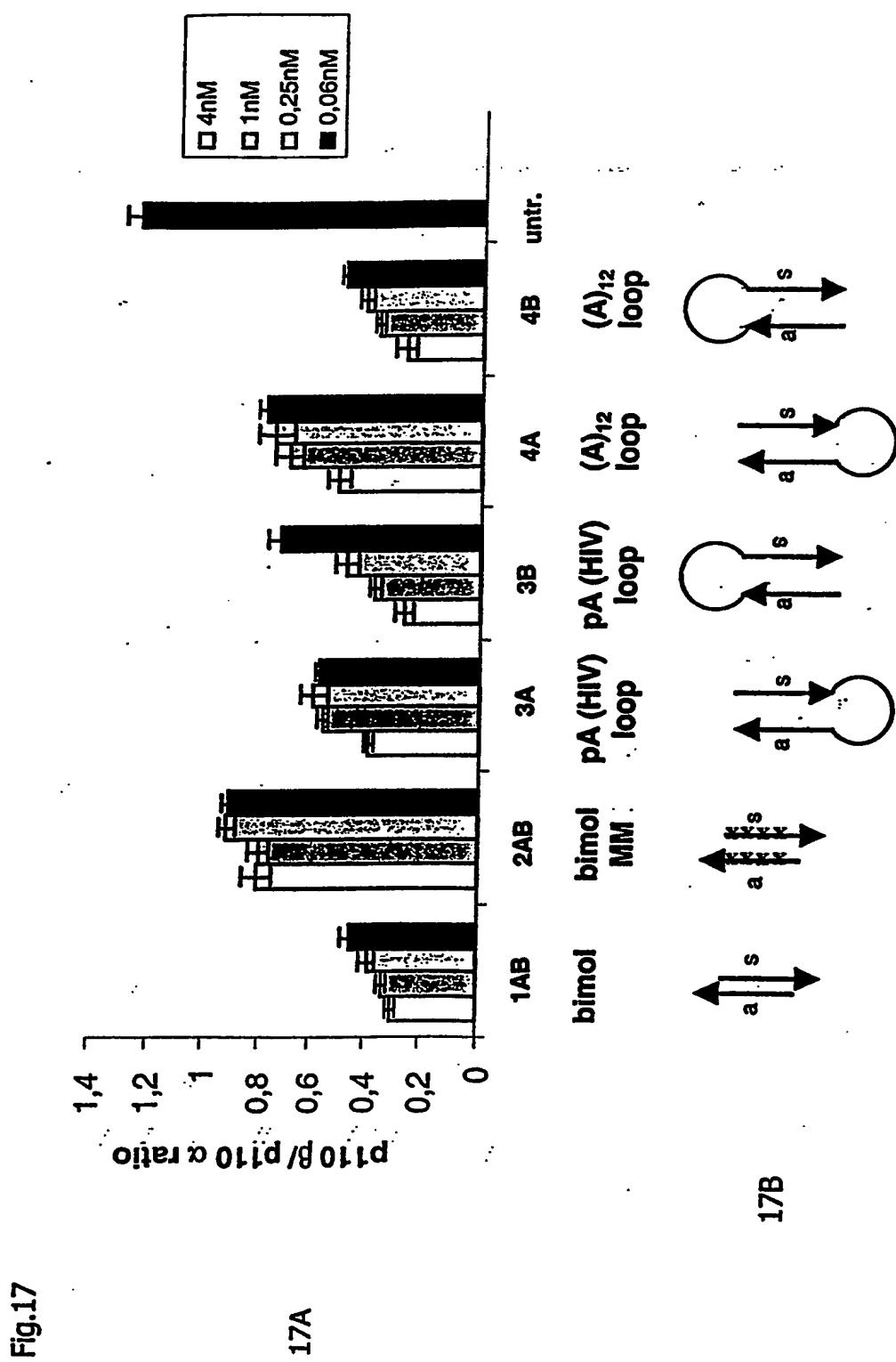
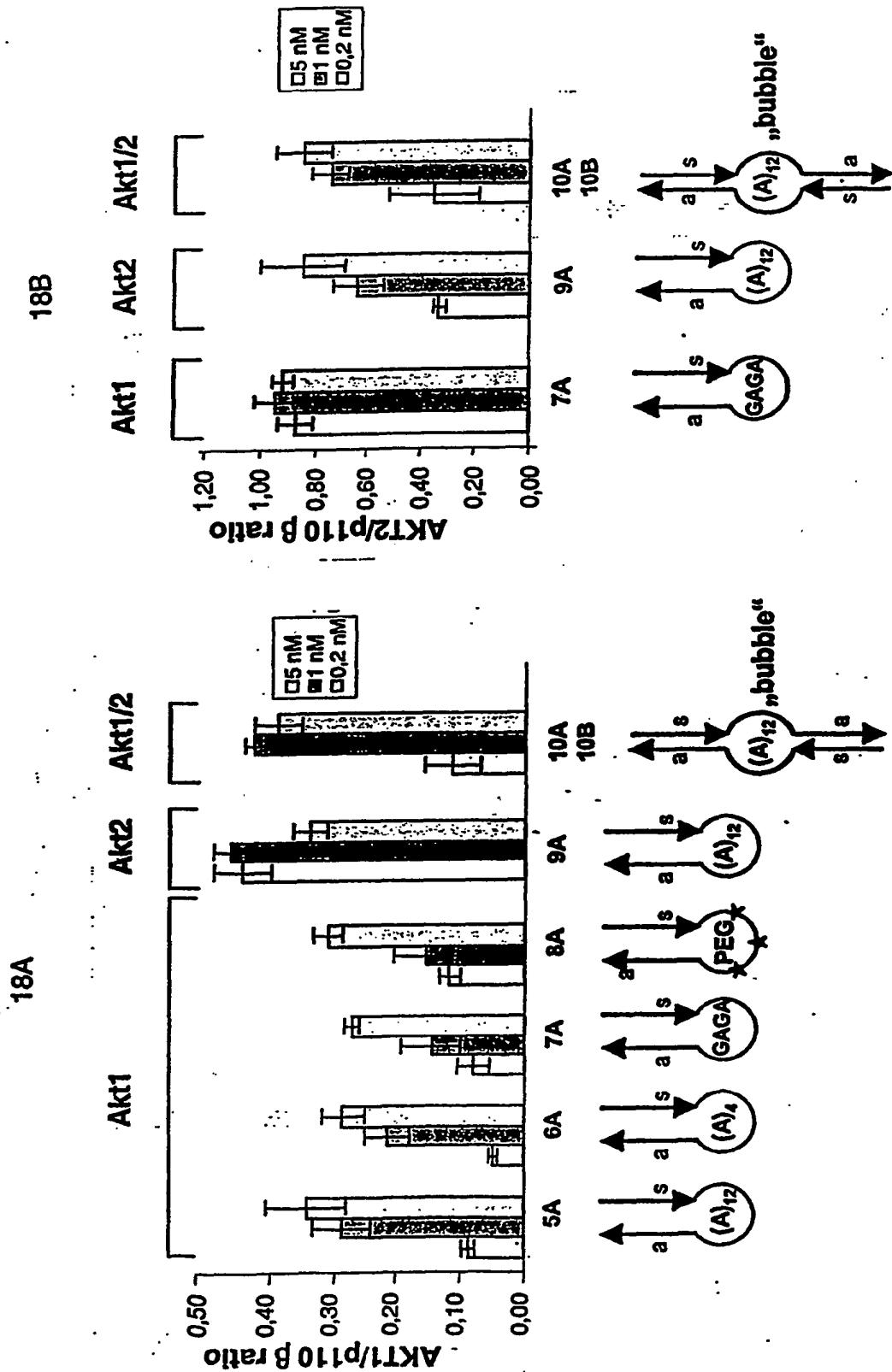
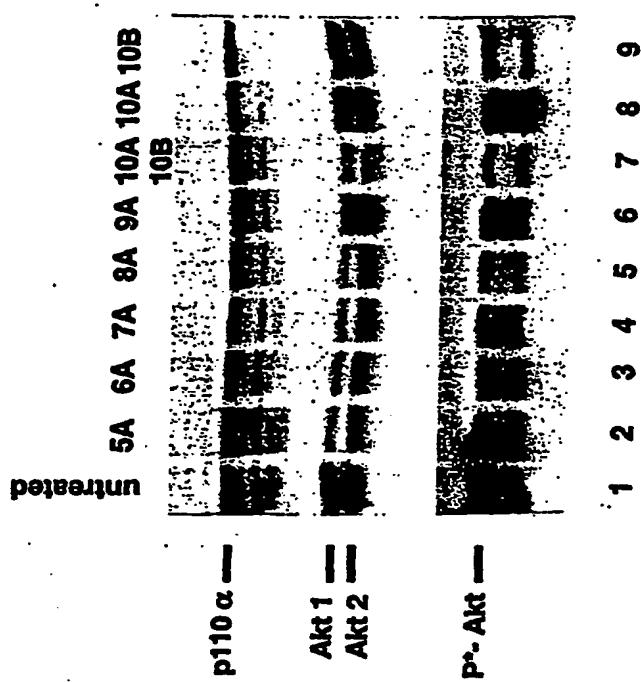


Fig. 18





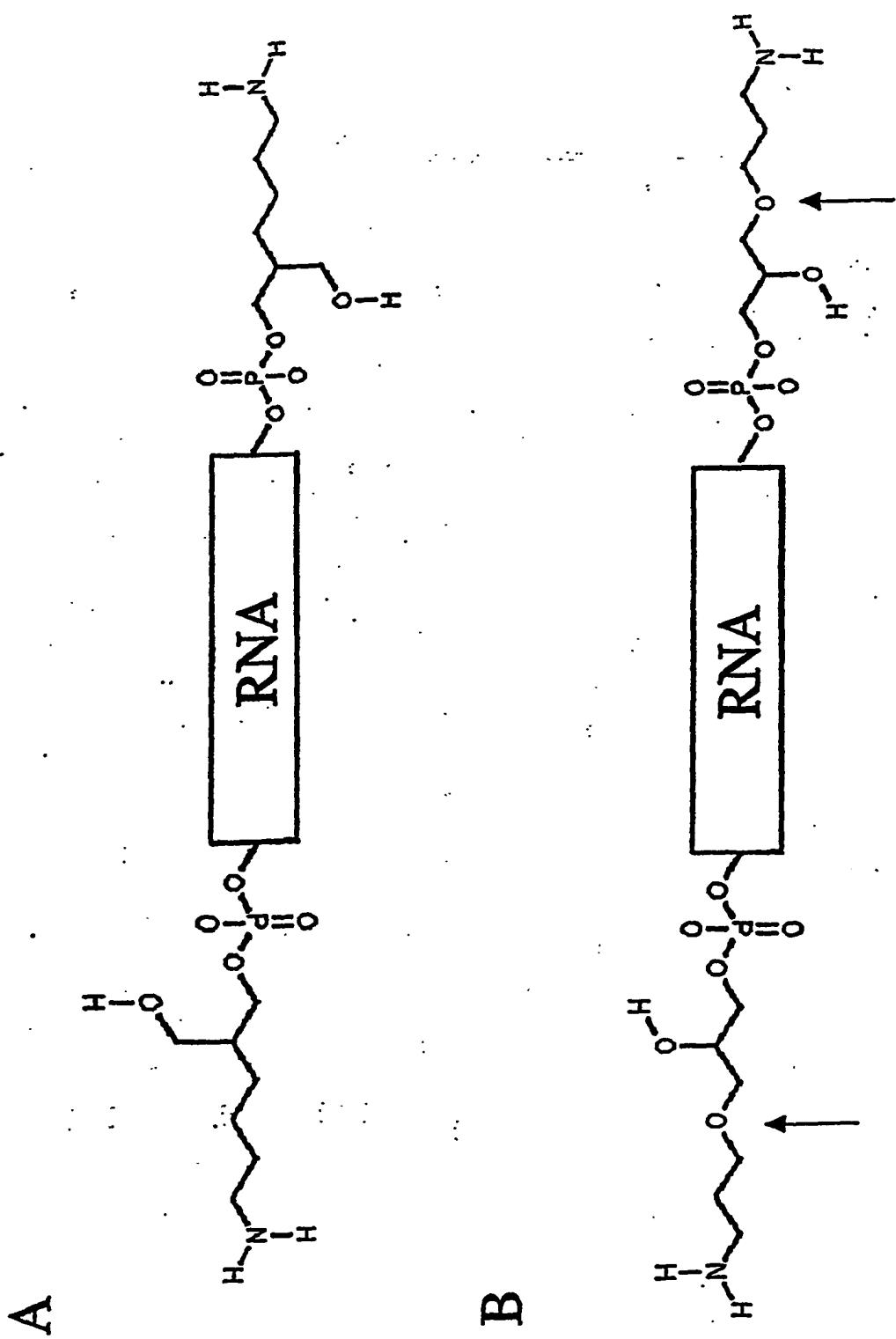


Fig. 19